FIG. 1A. DNA SEQUENCE OF HIGH MOLECULAR WEIGHT PROTEIN I (HMW1)

```
  1 ACAGCGTTCT CTTAATACTA GTACAAACCC ACAATAAAAT ATGACAAACA
 51 ACAATTACAA CACCTTTTTT GCAGTCTATA TGCAAATATT TTAAAAAATA
101 GTATAAATCC GCCATATAAA ATGGTATAAT CTTTCATCTT TCATCTTTCA
151 TCTTTCATCT TTCATCTTTC ATCTTTCATC TTTCATCTTT CATCTTTCAT
201 CTTTCATCTT TCATCTTTCA TCTTTCATCT TTCATCTTTC ACATGCCCTG
251 ATGAACCGAG GGAAGGGAGG GAGGGGCAAG AATGAAGAGG GAGCTGAACG
301 AACGCAAATG ATAAAGTAAT TTAATTGTTC AACTAACCTT AGGAGAAAAT
351 ATGAACAAGC TATATCGTCT CAAATTCAGC AAACGCCTGA ATGCTTTGGT
401 TGCTGTGTCT GAATTGGCAC GGGGTTGTGA CCATTCCACA GAAAAAGGCA
451 GCGAAAAACC TGCTCGCATG AAAGTGCGTC ACTTAGCGTT AAAGCCACTT
501 TCCGCTATGT TACTATCTTT AGGTGTAACA TCTATTCCAC AATCTGTTTT
551 AGCAAGCGGC TTACAAGGAA TGGATGTAGT ACACGGCACA GCCACTATGC
601 AAGTAGATGG TAATAAAACC ATTATCCGCA ACAGTGTTGA CGATATCATT
651 AATTGGAAAC AATTTAACAT CGACCAAAAT GAAATGGTGC AGTTTTTACA
701 AGAAAACAAC AACTCCGCCG TATTCAACCG TGTTACATCT AACCAAATCT
```

10092880.030802

FIG.1B.

```
751  CCCAATTAAA AGGGATTTTA GATTCTAACG GACAAGTCTT TTTAATCAAC
801  CCAAATGGTA TCACAATAGG TAAAGACGCA ATTATTAACA CTAATGGCTT
851  TACGGCTTCT ACGCTAGACA TTTCTAACGA AAACATCAAG GCGCGTAATT
901  TCACCTTCGA GCAAACCAAA GATAAAGCGC TCGCTGAAAT TGTGAATCAC
951  GGTTTAATTA CTGTCGGTAA AGACGGCAGT GTAAATCTTA TTGGTGGCAA
1001 AGTGAAAAAC GAGGGTGTGA TTAGCGTAAA TGGTGGCAGC ATTTCTTTAC
1051 TCGCAGGGCA AAAAATCACC ATCAGCGATA TAATAAACCC AACCATTACT
1101 TACAGCATTG CCGCGCCTGA AAATGAAGCG GTCAATCTGG GCGATATTTT
1151 TGCCAAAGGC GGTAACATTA ATGTCCGTGC TGCCACTATT CGAAACCAAG
1201 GTAAACTTTC TGCTGATTCT GTAAGCAAAG ATAAAAGCGG CAATATTGTT
1251 CTTTCCGCCA AAGAGGGTGA AGCGGAAATT GGCGGTGTAA TTTCCGCTCA
1301 AAATCAGCAA GCTAAAGGCG GCAAGCTGAT GATTACAGGC GATAAAGTCA
1351 CATTAAAAAC AGGTGCAGTT ATCGACCTTT CAGGTAAAGA AGGGGGAGAA
1401 ACTTACCTTG GCGGTGACGA GCGCGGCGAA GGTAAAAAGG GCATTCAATT
1451 AGCAAAGAAA ACCTCTTTAG AAAAAGGCTC AACCATCAAT GTATCAGGCA
1501 AAGAAAAAGG CGGACGCGCT ATTGTGTGGG GCGATATTGC GTTAATTGAC
```

10092880 .030802

FIG.1C.

```
1551  GGCAATATTA ACGCTCAAGG TAGTGGTGAT ATCGCTAAAA CCGGTGGTTT
1601  TGTGGAGACG TCGGGGCATG ATTTATTCAT CAAAGACAAT GCAATTGTTG
1651  ACGCCAAAGA GTGGTTGTTA GACCCGGATA ATGTATCTAT TAATGCAGAA
1701  ACAGCAGGAC GCAGCAATAC TTCAGAAGAC GATGAATACA CGGGATCCGG
1751  GAATAGTGCC AGCACCCCAA AACGAAACAA AGAAAAGACA ACATTAACAA
1801  ACACAACTCT TGAGAGTATA CTAAAAAAAG GTACCTTTGT TAACATCACT
1851  GCTAATCAAC GCATCTATGT CAATAGCTCC ATTAATTTAT CCAATGGCAG
1901  CTTAACTCTT TGGAGTGAGG GTCGGAGCGG TGGCGGCGTT GAGATTAACA
1951  ACGATATTAC CACCGGTGAT GATACCAGAG GTGCAAACTT AACAATTTAC
2001  TCAGGCGGCT GGGTTGATGT TCATAAAAAT ATCTCACTCG GGGCGCAAGG
2051  TAACATAAAC ATTACAGCTA AACAAGATAT CGCCTTTGAG AAAGGAAGCA
2101  ACCAAGTCAT TACAGGTCAA GGGACTATTA CCTCAGGCAA TCAAAAAGGT
2151  TTTAGATTTA ATAATGTCTC TCTAAACGGC ACTGGCAGCG GACTGCAATT
2201  CACCACTAAA AGAACCAATA AATACGCTAT CACAAATAAA TTTGAAGGGA
2251  CTTTAAATAT TTCAGGGAAA GTGAACATCT CAATGGTTTT ACCTAAAAAT
2301  GAAAGTGGAT ATGATAAATT CAAAGGACGC ACTTACTGGA ATTTAACCTC
```

FIG.1D.

```
2351  CTTAAATGTT TCCGAGAGTG GCGAGTTTAA CCTCACTATT GACTCCAGAC
2401  GAAGCGATAG TGCAGGCACA CTTACCCAGC CTTATAATTT AAACGGTATA
2451  TCATTCAACA AAGACACTAC CTTTAATGTT GAACGAAATG CAAGAGTCAA
2501  CTTTGACATC AAGGCACCAA TAGGGATAAA TAAGTATTCT AGTTTGAATT
2551  ACGCATCATT TAATGGAAAC ATTTCAGTTT CGGGAGGGGG GAGTGTTGAT
2601  TTCACACTTC TCGCCTCATC CTCTAACGTC CAAACCCCCG GTGTAGTTAT
2651  AAATTCTAAA TACTTTAATG TTTCAACAGG GTCAAGTTTA AGATTTAAAA
2701  CTTCAGGCTC AACAAAAACT GGCTTCTCAA TAGAGAAAGA TTTAACTTTA
2751  AATGCCACCG GAGGCAACAT AACACTTTTG CAAGTTGAAG GCACCGATGG
2801  AATGATTGGT AAAGGCATTG TAGCCAAAAA AAACATAACC TTTGAAGGAG
2851  GTAACATCAC CTTTGGCTCC AGGAAAGCCG TAACAGAAAT CGAAGGCAAT
2901  GTTACTATCA ATAACAACGC TAACGTCACT CTTATCGGTT CGGATTTTGA
2951  CAACCATCAA AAACCTTTAA CTATTAAAAA AGATGTCATC ATTAATAGCG
3001  GCAACCTTAC CGCTGGAGGC AATATTGTCA ATATAGCCGG AAATCTTACC
3051  GTTGAAAGTA ACGCTAATTT CAAAGCTATC ACAAATTTCA CTTTTAATGT
3101  AGGCGGCTTG TTTGACAACA AAGGCAATTC AAATATTTCC ATTGCCAAAG
3151  GAGGGGCTCG CTTTAAAGAC ATTGATAATT CCAAGAATTT AAGCATCACC
```


10090560 - 050502

FIG.1E.

```
3201  ACCAACTCCA GCTCCACTTA CCGCACTATT ATAAGCGGCA ATATAACCAA
3251  TAAAAACGGT GATTTAAATA TTACGAACGA AGGTAGTGAT ACTGAAATGC
3301  AAATTGGCGG CGATGTCTCG CAAAAAGAAG GTAATCTCAC GATTTCTTCT
3351  GACAAAATCA ATATTACCAA ACAGATAACA ATCAAGGCAG GTGTTGATGG
3401  GGAGAATTCC GATTCAGACG CGACAAACAA TGCCAATCTA ACCATTAAAA
3451  CCAAAGAATT GAAATTAACG CAAGACCTAA ATATTTCAGG TTTCAATAAA
3501  GCAGAGATTA CAGCTAAAGA TGGTAGTGAT TTAACTATTG GTAACACCAA
3551  TAGTGCTGAT GGTACTAATG CCAAAAAAGT AACCTTTAAC CAGGTTAAAG
3601  ATTCAAAAAT CTCTGCTGAC GGTCACAAGG TGACACTACA CAGCAAAGTG
3651  GAAACATCCG GTAGTAATAA CAACACTGAA GATAGCAGTG ACAATAATGC
3701  CGGCTTAACT ATCGATGCAA AAAATGTAAC AGTAAACAAC AATATTACTT
3751  CTCACAAAGC AGTGAGCATC TCTGCGACAA GTGGAGAAAT TACCACTAAA
3801  ACAGGTACAA CCATTAACGC AACCACTGGT AACGTGGAGA TAACCGCTCA
3851  AACAGGTAGT ATCCTAGGTG GAATTGAGTC CAGCTCTGGC TCTGTAACAC
3901  TTACTGCAAC CGAGGGCGCT CTTGCTGTAA GCAATATTTC GGGCAACACC
3951  GTTACTGTTA CTGCAAATAG CGGTGCATTA ACCACTTTGG CAGGCTCTAC
```


WO 95/05850 PCT/US94/09575

FIG.1F.

```
4001  AATTAAAGGA ACCGAGAGTG TAACCACTTC AAGTCAATCA GGCGATATCG
4051  GCGGTACGAT TTCTGGTGGC ACAGTAGAGG TTAAAGCAAC CGAAAGTTTA
4101  ACCACTCAAT CCAATTCAAA AATTAAAGCA ACAACAGGCG AGGCTAACGT
4151  AACAAGTGCA ACAGGTACAA TTGGTGGTAC GATTTCCGGT AATACGGTAA
4201  ATGTTACGGC AAACGCTGGC GATTTAACAG TTGGGAATGG CGCAGAAATT
4251  AATGCGACAG AAGGAGCTGC AACCTTAACT ACATCATCGG GCAAATTAAC
4301  TACCGAAGCT AGTTCACACA TTACTTCAGC CAAGGGTCAG GTAAATCTTT
4351  CAGCTCAGGA TGGTAGCGTT GCAGGAAGTA TTAATGCCGC CAATGTGACA
4401  CTAAATACTA CAGGCACTTT AACTACCGTG AAGGGTTCAA ACATTAATGC
4451  AACCAGCGGT ACCTTGGTTA TTAACGCAAA AGACGCTGAG CTAAATGGCG
4501  CAGCATTGGG TAACCACACA GTGGTAAATG CAACCAACGC AAATGGCTCC
4551  GGCAGCGTAA TCGCGACAAC CTCAAGCAGA GTGAACATCA CTGGGGATTT
4601  AATCACAATA AATGGATTAA ATATCATTTC AAAAAACGGT ATAAACACCG
4651  TACTGTTAAA AGGCGTTAAA ATTGATGTGA AATACATTCA ACCGGGTATA
4701  GCAAGCGTAG ATGAAGTAAT TGAAGCGAAA CGCATCCTTG AGAAGGTAAA
4751  AGATTTATCT GATGAAGAAA GAGAAGCGTT AGCTAAACTT GGAGTAAGTG
4801  CTGTACGTTT TATTGAGCCA AATAATACAA TTACAGTCGA TACACAAAAT
```


EP 0 663 956 B1

FIG.1G.

```
4851  GAATTTGCAA CCAGACCATT AAGTCGAATA GTGATTTCTG AAGGCAGGGC
4901  GTGTTTCTCA AACAGTGATG GCGCGACGGT GTGCGTTAAT ATCGCTGATA
4951  ACGGGCGGTA GCGGTCAGTA ATTGACAAGG TAGATTTCAT CCTGCAATGA
5001  AGTCATTTTA TTTTCGTATT ATTTACTGTG TGGGTTAAAG TTCAGTACGG
5051  GCTTTACCCA TCTTGTAAAA AATTACGGAG AATACAATAA AGTATTTTTA
5101  ACAGGTTATT ATTATG
```


SUBSTITUTE SHEET (RULE 26)

FIG. 2A. AMINO ACID SEQUENCE OF HIGH MOLECULAR WEIGHT PROTEIN I

```
  1  MNKIYRLKFS KRLNALVAVS ELARGCDHST EKGSEKPARM KVRHLALKPL
 51  SAMLLSLGVT SIPQSVLASG LQGMDVVHGT ATMQVDGNKT IIRNSVDAII
101  NWKQFNIDQN EMVQFLQENN NSAVFNRVTS NQISQLKGIL DSNGQVFLIN
151  PNGITIGKDA IINTNGFTAS TLDISNENIK ARNFTFEQTK DKALAEIVNH
201  GLITVGKDGS VNLIGGKVKN EGVISVNGGS ISLLAGQKIT ISDIINPTIT
251  YSIAAPENEA VNLGDIFAKG GNINVRAATI RNQGKLSADS VSKDKSGNIV
301  LSAKEGEAEI GGVISAQNQQ AKGGKLMITG DKVTLKTGAV IDLSGKEGGE
351  TYLGGDERGE GKNGIQLAKK TSLEKGSTIN VSGKEKGGRA IVWGDIALID
401  GNINAQGSGD IAKTGGFVET SGHDLFIKDN AIVDAKEWLL DFDNVSINAE
451  TAGRSNTSED DEYTGSGNSA STPKRNKEKT TLTNTTLESI LKKGTFVNIT
501  ANQRIYVNSS INLSNGSLTL WSEGRSGGGV EINNDITTGD DTRGANLTIY
551  SGGWVDVHKN ISLGAQGNIN ITAKQDIAFE KGSNQVITGQ GTITSGNQKG
601  FRFNNVSLNG TGSGLQFTTK RTNKYAITNK FEGTLNISGK VNISMVLPKN
651  ESGYDKFKGR TYWNLTSLNV SESGEFNLTI DSRGSDSAGT LTQPYNLNGI
701  SFNKDTTFNV ERNARVNFDI KAPIGINKYS SLNYASFNGN ISVSGGGSVD
```


EP 0 068 637 B1

10092880.030802

FIG. 2B.

751	FTLLASSSNV	QTPGVVINSK	YFNVSTGSSL	RFKTSGSTKT	GFSIEKDLTL
801	NATGGNITLL	QVEGTDGMIG	KGIVAKKNIT	FEGGNITFGS	RKAVTEIEGN
851	VTINNNANVT	LIGSDFDNHQ	KPLTIKKDVI	INSGNLTAGG	NIVNIAGNLT
901	VESNANFKAI	TNFTFNVGGL	FDNKGNSNIS	IAKGGARFKD	IDNSKNLSIT
951	TNSSSTYRTI	ISGNITNKNG	DLNITNEGSD	TEMQIGGDVS	QKEGNLTISS
1001	DKINITKQIT	IKAGVDGENS	DSDATNNANL	TIKTKELKLT	QDLNISGFNK
1051	AEITAKDGSD	LTIGNTNSAD	GTNAKKVTFN	QVKDSKISAD	GHKVTLHSKV
1101	ETSGSNNNTE	DSSDNNAGLT	IDAKNVTVNN	NITSHKAVSI	SATSGEITTK
1151	TGTTINATTG	NVEITAQTGS	ILGGIESSSG	SVTLTATEGA	LAVSNISGNT
1201	VTVTANSGAL	TTLAGSTIKG	TESVTTSSQS	GDIGGTISGG	TVEVKATESL
1251	TTQSNSKIKA	TTGEANVTSA	TGTIGGTISG	NTVNVTANAG	DLTVGNGAEI
1301	NATEGAATLT	TSSGKLTTEA	SSHITSAKGQ	VNLSAQDGSV	AGSINAANVT
1351	LNTTGTLTTV	KGSNINATSG	TLVINAKDAE	LNGAALGNHT	VVNATNANGS
1401	GSVIATTSSR	VNITGDLITI	NGLNIISKNG	INTVLLKGVK	IDVKYIQPGI
1451	ASVDEVIEAK	RILEKVKDLS	DEEREALAKL	GVSAVRFIEP	NNTITVDTQN
1501	EFATRPLSRI	VISEGRACFS	NSDGATVCVN	IADNGR	

10092880.030802

FIG.3A. DNA SEQUENCE OF HIGH MOLECULAR WEIGHT PROTEIN II (HMW2)

```
  1 TAAATATACA AGATAATAAA AATAAATCAA GATTTTTGTG ATGACAAACA
 51 ACAATTACAA CACCTTTTTT GCAGTCTATA TGCAAATATT TTAAAAAAAT
101 AGTATAAATC CGCCATATAA AATGGTATAA TCTTTCATCT TTCATCTTTA
151 ATCTTTCATC TTTCATCTTT CATCTTTCAT CTTTCATCTT TCATCTTTCA
201 TCTTTCATCT TTCATCTTTC ATCTTTCATC TTTCATCTTT CACATGAAAT
251 GATGAACCGA GGGAAGGGAG GGAGGGGCAA GAATGAAGAG GGAGCTGAAC
301 GAACGCAAAT GATAAAGTAA TTTAATTGTT CAACTAACCT TAGGAGAAAA
351 TATGAACAAG ATATATCGTC TCAAATTCAG CAAACGCCTG AATGCTTTGG
401 TTGCTGTGTC TGAATTGGCA CGGGGTTGTG ACCATTCCAC AGAAAAAGGC
451 TTCCGCTATG TTACTATCTT TAGGTGTAAC CACTTAGCGT TAAAGCCACT
501 TTCCGCTATG TTACTATCTT TAGGTGTAAC ATCTATTCCA CAATCTGTTT
551 TAGCAAGCGG CTTACAAGGA ATGGATGTAG TACACGGCAC AGCCACTATG
601 CAAGTAGATG GTAATAAAAC CATTATCCGC AACAGTGTTG ACGCTATCAT
651 TAATTGGAAA CAATTTAACA TCGACCAAAA TGAAATGGTG CAGTTTTTAC
701 AAGAAAACAA CAACTCCGCC GTATTCAACC GTGTTACATC TAACCAAATC
```

10092880 .030802

FIG. 3B.

751	TCCCAATTAA	AAGGGATTTT	AGATTCTAAC	GGACAAGTCT	TTTTAATCAA
801	CCCAAATGGT	ATCACAATAG	GTAAAGACGC	AATTATTAAC	ACTAATGGCT
851	TTACGGCTTC	TACGCTAGAC	ATTTCTAACG	AAAACATCAA	GGCGCGTAAT
901	TTCACCTTCG	AGCAAACCAA	AGATAAAGCG	CTCGCTGAAA	TTGTGAATCA
951	CGGTTTAATT	ACTGTCGGTA	AAGACGGCAG	TGTAAATCTT	ATTGGTGGCA
1001	AAGTGAAAAA	CGAGGGTGTG	ATTAGCGTAA	ATGGTGGCAG	CATTTCTTTA
1051	CTCGCAGGGC	AAAAAATCAC	CATCAGCGAT	ATAATAAACC	CAACCATTAC
1101	TTACAGCATT	GCCGCGCCTG	AAAATGAAGC	GGTCAATCTG	GGCGATATTT
1151	TTGCCAAAGG	CGGTAACATT	AATGTCCGTG	CTGCCACTAT	TCGAAACCAA
1201	GGTAAACTTT	CTGCTGATTC	TGTAAGCAAA	GATAAAAGCG	GCAATATTGT
1251	TCTTTCCGCC	AAAGAGGGTG	AAGCGGAAAT	TGGCGGTGTA	ATTTCCGCTC
1301	AAAATCAGCA	AGCTAAAGGC	GGCAAGCTGA	TGATTACAGG	CGATAAAGTC
1351	ACATTAAAAA	CAGGTGCAGT	TATCGACCTT	TCAGGTAAAG	AAGGGGGAGA
1401	AACTTACCTT	GGCGGTGACG	AGCGCGGCGA	AGGTAAAAAC	GGCATTCAAT
1451	TAGCAAAGAA	AACCTCTTTA	GAAAAAGGCT	CAACCATCAA	TGTATCAGGC
1501	AAAGAAAAAG	GCGGACGCGC	TATTGTGTGG	GGCGATATTG	CGTTAATTGA

FIG.3C.

```
1551  CGGCAATATT AACGCTCAAG GTAGTGGTGA TATCGCTAAA ACCGGTGGTT
1601  TTGTGGAGAC ATCGGGGCAT TATTTATCCA TTGACAGCAA TGCAATTGTT
1651  AAAACAAAAG AGTGGTTGCT AGACCCTGAT GATGTAACAA TTGAAGCCGA
1701  AGACCCCCTT CGCAATAATA CCGGTATAAA TGATGAATTC CCAACAGGCA
1751  CCGGTGAAGC AAGCGACCCT AAAAAAAATA GCGAACTCAA AACAACGCTA
1801  ACCAATACAA CTATTTCAAATTATCTGAAA AACGCCTGGA CAATGAATAT
1851  AACGGCATCA AGAAAACTTA CCGTTAATAG CTCAATCAAC ATCGGAAGCA
1901  ACTCCCACTT AATTCTCCAT AGTAAAGGTC AGCGTGGCGG AGGCGTTCAG
1951  ATTGATGGAG ATATTACTTC TAAAGGCGGA AATTTAACCA TTTATTCTGG
2001  CGGATGGGTT GATGTTCATA AAAATATTAC GCTTGATCAG GGTTTTTTAA
2051  ATATTACCGC CGCTTCCGTA GCTTTTGAAG GTGGAAATAA CAAAGCACGC
2101  GACGCGGCAA ATGCTAAAAT TGTCGCCCAG GGCACTGTAA CCATTACAGG
2151  AGAGGGAAAA GATTTCAGGG CTAACAACGT ATCTTTAAAC GGAACGGGTA
2201  AAGGTCTGAA TATCATTTCA TCAGTGAATA ATTTAACCCA CAATCTTAGT
2251  GGCACAATTA ACATATCTGG GAATATAACA ATTAACCAAA CTACGAGAAA
2301  GAACACCTCG TATTGGCAAA CCAGCCATGA TTCGCACTGG AACGTCAGTG
2351  CTCTTAATCT AGAGACAGGC GCAAATTTTA CCTTTATTAA ATACATTTCA
```


SUBSTITUTE SHEET (RULE 26)

FIG.3D.

```
2401  AGCAATAGCA AAGGCTTAAC AACACAGTAT AGAAGCTCTG CAGGGGTGAA
2451  TTTTAACGGC GTAAATGGCA ACATGTCATT CAATCTCAAA GAAGGAGCGA
2501  AAGTTAATTT CAAATTAAAA CCAAACGAGA ACATGAACAC AAGCAAACCT
2551  TTACCAATTC GGTTTTTAGC CAATATCACA GCCACTGGTG GGGGCTCTGT
2601  TTTTTTTGAT ATATATGCCA ACCATTCTGG CAGAGGGGCT GAGTTAAAAA
2651  TGAGTGAAAT TAATATCTCT AACGGCGCTA ATTTTACCTT AAATTCCCAT
2701  GTTCGCGGCG ATGACGCTTT TAAAATCAAC AAAGACTTAA CCATAAATGC
2751  AACCAATTCA AATTTCAGCC TCAGACAGAC GAAAGATGAT TTTTATGACG
2801  GGTACGCACG CAATGCCATC AATTCAACCT ACAACATATC CATTCTGGGC
2851  GGTAATGTCA CCCTTGGTGG ACAAAACTCA AGCAGCAGCA TTACGGGGAA
2901  TATTACTATC GAGAAAGCAG CAAATGTTAC GCTAGAAGCC AATAACGCCC
2951  CTAATCAGCA AAACATAAGG GATAGAGTTA TAAAACTTGG CAGCTTGCTC
3001  GTTAATGGGA GTTTAAGTTT AACTGGCGAA AATGCAGATA TTAAAGGCAA
3051  TCTCACTATT TCAGAAAGCG CCACTTTTAA AGGAAAGACT AGAGATACCC
3101  TAAATATCAC CGGCAATTTT ACCAATAATG GCACTGCCGA AATTAATATA
3151  ACACAAGGAG TGGTAAAACT TGGCAATGTT ACCAATGATG GTGATTTAAA
```


SUBSTITUTE SHEET (RULE 26)

10092880.030802

FIG.3E.

3201	CATTACCACT	CACGCTAAAC	GCAACCAAAG	AAGCATCATC	GGCGGAGATA
3251	TAATCAACAA	AAAAGGAAGC	TTAAATATTA	CAGACAGTAA	TAATGATGCT
3301	GAAATCCAAA	TTGGCGGCAA	TATCTCGCAA	AAAGAAGGCA	ACCTCACGAT
3351	TTCTTCCGAT	AAAATTAATA	TCACCAAACA	GATAACAATC	AAAAAGGGTA
3401	TTGATGGAGA	GGACTCTAGT	TCAGATGCGA	CAAGTAATGC	CAACCTAACT
3451	ATTAAAACCA	AAGAATTGAA	ATTGACAGAA	GACCTAAGTA	TTTCAGGTTT
3501	CAATAAAGCA	GAGATTACAG	CCAAAGATGG	TAGAGATTTA	ACTATTGGCA
3551	ACAGTAATGA	CGGTAACAGC	GGTGCCGAAG	CCAAAACAGT	AACTTTTAAC
3601	AATGTTAAAG	ATTCAAAAAT	CTCTGCTGAC	GGTCACAATG	TGACACTAAA
3651	TAGCAAAGTG	AAAACATCTA	GCAGCAATGG	CGGACGTGAA	AGCAATAGCG
3701	ACAACGATAC	CGGCTTAACT	ATTACTGCAA	AAAATGTAGA	AGTAAACAAA
3751	GATATTACTT	CTCTCAAAAC	AGTAAATATC	ACCGCGTCGG	AAAAGGTTAC
3801	CACCACAGCA	GGCTCGACCA	TTAACGCAAC	AAATGGCAAA	GCAAGTATTA
3851	CAACCAAAAC	AGGTGATATC	AGCGGTACGA	TTTCCGGTAA	CACGGTAAGT
3901	GTTAGCGCGA	CTGGTGATTT	AACCACTAAA	TCCGGCTCAA	AAATTGAAGC
3951	GAAATCGGGT	GAGGCTAATG	TAACAAGTGC	AACAGGTACA	ATTGGCGGTA

FIG.3F.

```
4001  CAATTTCCGG TAATACGGTA AATGTTACGG CAAACGCTGG CGATTTAACA
4051  GTTGGGAATG GCGCAGAAAT TAATGCGACA GAAGGAGCTG CAACCTTAAC
4101  CGCAACAGGG AATACCTTGA CTACTGAAGC CGGTTCTAGC ATCACTTCAA
4151  CTAAGGGTCA GGTAGACCTC TTGGCTCAGA ATGGTAGCAT CGCAGGAAGC
4201  ATTAATGCTG CTAATGTGAC ATTAAATACT ACAGGCACCT TAACCACCGT
4251  GGCAGGCTCG GATATTAAAG CAACCAGCGG CACCTTGGTT ATTAACGCAA
4301  AAGATGCTAA GCTAAATGGT GATGCATCAG GTGATAGTAC AGAAGTGAAT
4351  GCAGTCAACG CAAGCGGCTC TGGTAGTGTG ACTGCGGCAA CCTCAAGCAG
4401  TGTGAATATC ACTGGGGATT TAAACACAGT AAATGGGTTA AATATCATTT
4451  CGAAAGATGG TAGAAACACT GTGCGCTTAA GAGGCAAGGA AATTGAGGTG
4501  AAATATATCC AGCCAGGTGT AGCAAGTGTA GAAGAAGTAA TTGAAGCGAA
4551  ACGCGTCCTT GAAAAAGTAA AAGATTTATC TGATGAAGAA AGAGAAACAT
4601  TAGCTAAACT TGGTGTAAGT GCTGTACGTT TTGTTGAGCC AAATAATACA
4651  ATTACAGTCA ATACACAAAA TGAATTTACA ACCAGACCGT CAAGTCAAGT
4701  GATAATTTCT GAAGGTAAGG CGTGTTTCTC AAGTGGTAAT GGCGCACGAG
4751  TATGTACCAA TGTTGCTGAC GATGGACAGC CGTAGTCAGT AATTGACAAG
4801  GTAGATTTCA TCCTGCAATG AAGTCATTTT ATTTTCGTAT TATTTACTGT
```


10095880.050902

FIG.3G.

```
4851  GTGGGTTAAA GTTCAGTACG GGCTTTACCC ATCTTGTAAA AAATTACGGA
4901  GAATACAATA AAGTATTTTT AACAGGTTAT TATTATG
```

FIG.4A. AMINO ACID SEQUENCE OF HIGH MOLECULAR WEIGHT PROTEIN 2

```
  1  MNKIYRLKFS KRLNALVAVS ELARGCDHST EKGSEKPARM KVRHLALKPL
 51  SAMLLSLGVT SIPQSVLASG LQGMDVVHGT ATMQVDGNKT IIRNSVDAII
101  NWKQFNIDQN EMVQFLQENN NSAVFNRVTS NQISQLKGIL DSNGQVFLIN
151  PNGITIGKDA IINTNGFTAS TLDISNENIK ARNFTFEQTK DKALAEIVNH
201  GLITVGKDGS VNLIGGKVKN EGVISVNGGS ISLLAGQKIT ISDIINPTIT
251  YSIAAPENEA VNLGDIFAKG GNINVRAATI RNQGKLSADS VSKDKSGNIV
301  LSAKEGEAEI GGVISAQNQQ AKGGKLMITG DKVTLKTGAV IDLSGKEGGE
351  TYLGGDERGE GKNGIQLAKK TSLEKGSTIN VSGKEKGGRA IVWGDIALID
401  GNINAQGSGD IAKTGGFVET SGHDLFIKDN AIVDAKEWLL DFDNVSINAE
451  DPLRNNTGIN DEFPTGTGEA SDPKKNSELK TTLTNTTISN YLKNAWTMNI
501  TASRKLTVNS SINIGSNSHL ILHSKGQRGG GVQIDGDITS KGGNLTIYSG
551  GWVDVHKNIT LDQGFLNITA ASVAFEGGNN KARDAANAKI VAQGTVTITG
601  EGKDFRANNV SLNGTGKGLN IISSVNNLTH NLSGTINISG NITINQTTRK
651  NTSYWQTSHD SHWNVSALNL ETGANFTFIK YISSNSKGLT TQYRSSAGVN
701  FNGVNGNMSF NLKEGAKVNF KLKPNENMNT SKPLPIRFLA NITATGGGSV
```


WO 2005/032460 PCT/US2004/032460

10092880 .030802

FIG. 4B.

```
751   FFDIYANHSG RGAELKMSEI NISNGANFTL NSHVRGDDAF KINKDLTINA
801   TNSNFSLRQT KDDFYDGYAR NAINSTYNIS ILGGNVTLGG QNSSSSITGN
851   ITIEKAANVT LEANNAPNQQ NIRDRVIKLG SLLVNGSLSL TGENADIKGN
901   LTISESATFK GKTRDTLNIT GNFTNNGTAE INITQGVVKL GNVTNDGDLN
951   ITTHAKRNQR SIIGGDIINK KGSLNITDSN NDAEIQIGGN ISQKEGNLTI
1001  SSDKINITKQ ITIKKGIDGE DSSSDATSNA NLTIKTKELK LTEDLSISGF
1051  NKAEITAKDG RDLTIGNSND GNSGAEAKTV TFNNVKDSKI SADGHNVTLN
1101  SKVKTSSSNG GRESNSDNDT GLTITAKNVE VNKDITSLKT VNITASEKVT
1151  TTAGSTINAT NGKASITTKT GDISGTISGN TVSVSATVDL TTKSGSKIEA
1201  KSGEANVTSA TGTIGGTISG NTVNVTANAG DLTVGNGAEI NATEGAATLT
1251  ATGNTLTTEA GSSITSTKGQ VDLLAQNGSI AGSINAANVT LNTTGTLTTV
1301  AGSDIKATSG TLVINAKDAK LNGDASGDST EVNAVNASGS GSVTAATSSS
1351  VNITGDLNTV NGLNIISKDG RNTVRLRGKE IEVKYIQPGV ASVEEVIEAK
1401  RVLEKVKDLS DEERETLAKL GVSAVRFVEP NNTITVNTQN EFTTRPSSQV
1451  IISEGKACFS SGNGARVCTN VADDGQP
```

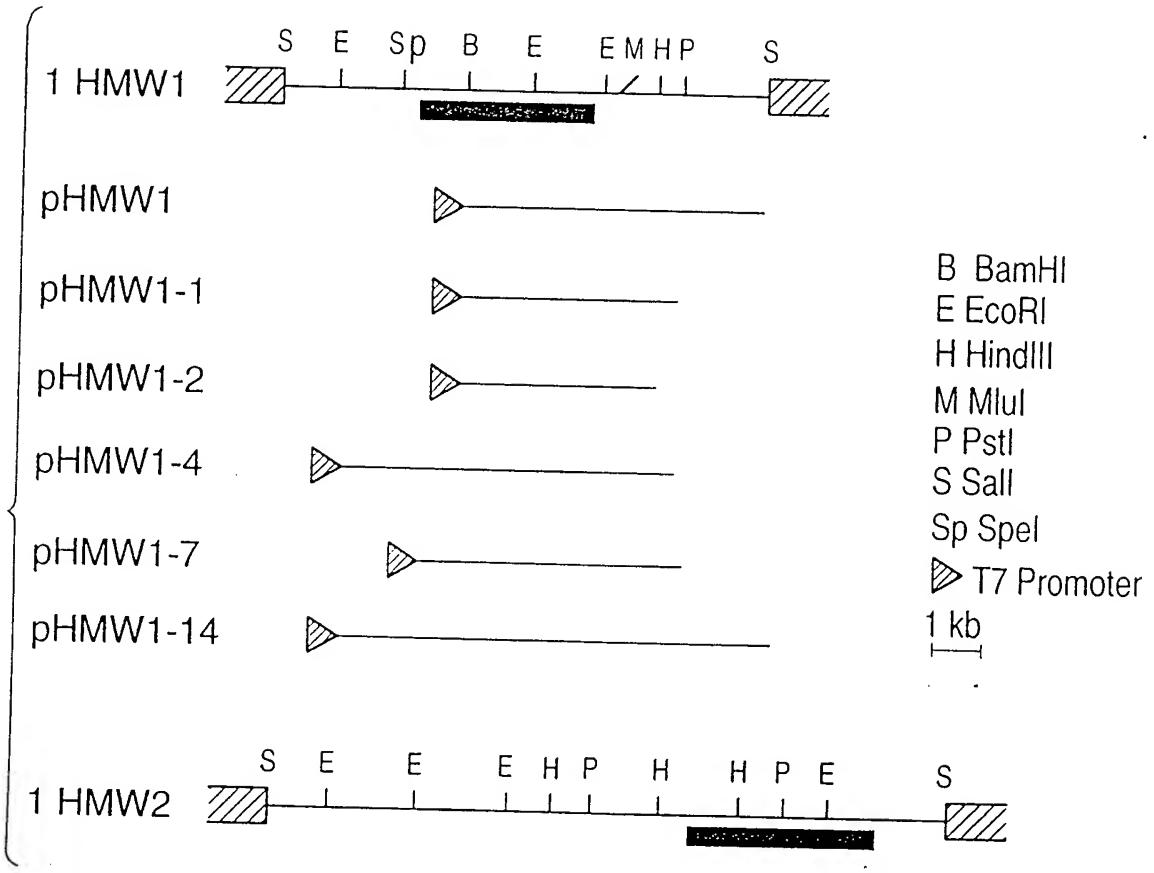

1 HMW1
S E Sp B E E M H P S
pHMW1
pHMW1-1
pHMW1-2
pHMW1-4
pHMW1-7
pHMW1-14
B BamHI
E EcoRI
H HindIII
M MluI
P PstI
S SalI
Sp SpeI
T7 Promoter
1 kb
1 HMW2
S E E E H P H H P E S

FIG.5A.

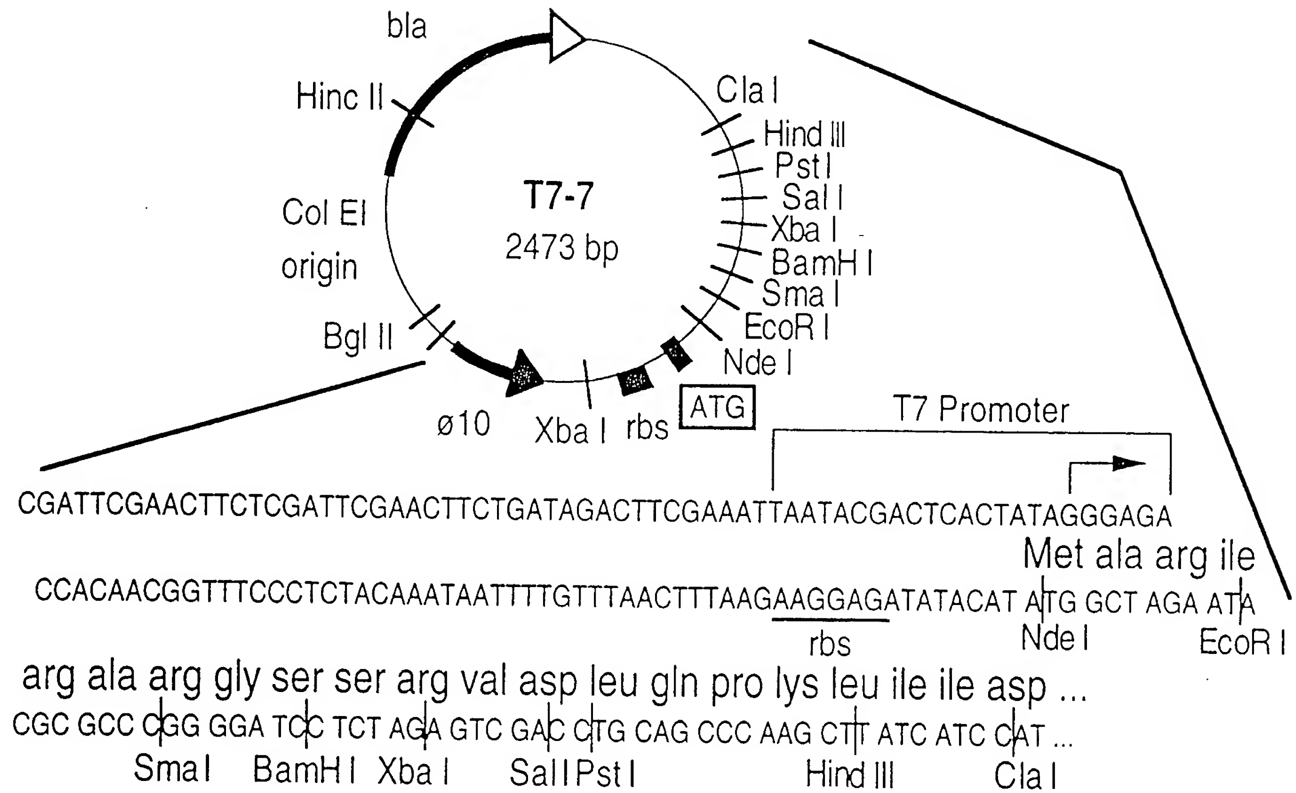


FIG. 5B.

(A) Partial restriction maps of representative HMW1 and HMW2 recombinant phage and of HMW1 plasmid subclones. The shaded boxes indicate the locations of the structural genes. In the recombinant phage, transcription proceeds from left to right for the HMW1 gene and from right to left for the HMW2 gene. The methods used for construction of the plasmids shown are described in the text. (B) Restriction map of the T7 expression vector pT7-7. This vector contains the T7 RNA polymerase promoter ϕ10, a ribosome - binding site (rbs), and the translational start site for the T7 gene 10 protein upstream from a multiple cloning site (37).

10092880 .030802

FIG.6A.

```
   1  ACAGCGTTCT CTTAATACTA GTACAAACCC ACAATAAAAT ATGACAAACA
  51  ACAATTACAA CACCTTTTTT GCAGTCTATA TGCAAATATT TTAAAAAATA
 101  GTATAAATCC GCCATATAAA ATGGTATAAT CTTTCATCTT TCATCTTTCA
 151  TCTTTCATCT TTCATCTTTC ATCTTTCATC TTTCATCTTT CATCTTTCAT
 201  CTTTCATCTT TCATCTTTCA TCTTTCATCT TTCATCTTTC ACATGAAATG
 251  ATGAACCGAG GGAAGGGAGG GAGGGGCAAG AATGAAGAGG GAGCTGAACG
 301  AACGCAAATG ATAAAGTAAT TTAATTGTTC AACTAACCTT AGGAGAAAAT
 351  ATGAACAAGA TATATCGTCT CAAATTCAGC AAACGCCTGA ATGCTTTGGT
 401  TGCTGTGTCT GAATTGGCAC GGGGTTGTGA CCATTCCACA GAAAAAGGCA
 451  GCGAAAAACC TGCTCGCATG AAAGTGCGTC ACTTAGCGTT AAAGCCACTT
 501  TCCGCTATGT TACTATCTTT AGGTGTAACA TCTATTCCAC AATCTGTTTT
 551  AGCAAGCGGC TTACAAGGAA TGGATGTAGT ACACGGCACA GCCACTATGC
 601  AAGTAGATGG TAATAAAACC ATTATCCGCA ACAGTGTTGA CGCTATCATT
 651  AATTGGAAAC AATTTAACAT CGACCAAAAT GAAATGGTGC AGTTTTTACA
 701  AGAAAACAAC AACTCCGCCG TATTCAACCG TGTTACATCT AACCAAATCT
 751  CCCAATTAAA AGGGATTTTA GATTCTAACG GACAAGTCTT TTTAATCAAC
```


SUBSTITUTE SHEET (RULE 26)

FIG.6B.

801	CCAAATGGTA	TCACAATAGG	TAAAGACGCA	ATTATTAACA	CTAATGGCTT
851	TACGGCTTCT	ACGCTAGACA	TTTCTAACGA	AAACATCAAG	GCGCGTAATT
901	TCACCTTCGA	GCAAACCAAA	GATAAAGCGC	TCGCTGAAAT	TGTGAATCAC
951	GGTTTAATTA	CTGTCGGTAA	AGACGGCAGT	GTAAATCTTA	TTGGTGGCAA
1001	AGTGAAAAAC	GAGGGTGTGA	TTAGCGTAAA	TGGTGGCAGC	ATTTCTTTAC
1051	TCGCAGGGCA	AAAAATCACC	ATCAGCGATA	TAATAAACCC	AACCATTACT
1101	TACAGCATTG	CCGCGCCTGA	AAATGAAGCG	GTCAATCTGG	GCGATATTTT
1151	TGCCAAAGGC	GGTAACATTA	ATGTCCGTGC	TGCCACTATT	CGAAACCAAG
1251	CTTTCCGCCA	AAGAGGGTGA	AGCGGAAATT	GGCGGTGTAA	TTTCCGCTCA
1301	AAATCAGCAA	GCTAAAGGCG	GCAAGCTGAT	GATTACAGGC	GATAAAGTCA
1351	CATTAAAAAC	AGGTGCAGTT	ATCGACCTTT	CAGGTAAAGA	AGGGGGAGAA
1401	ACTTACCTTG	GCGGTGACGA	GCGCGGCGAA	GGTAAAAACG	GCATTCAATT
1451	AGCAAAGAAA	ACCTCTTTAG	AAAAAGGCTC	AACCATCAAT	GTATCAGGCA
1501	AAGAAAAAGG	CGGACGCGCT	ATTGTGTGGG	GCGATATTGC	GTTAATTGAC
1551	GGCAATATTA	ACGCTCAAGG	TAGTGGTGAT	ATCGCTAAAA	CCGGTGGTTT
1601	TGTGGAGACG	TCGGGGCATG	ATTTATTCAT	CAAAGACAAT	GCAATTGTTG

10092880.030802

FIG.6C.

```
1651  ACGCCAAAGA GTGGTTGTTA GACCCGGATA ATGTATCTAT TAATGCAGAA
1701  ACAGCAGGAC GCAGCAATAC TTCAGAAGAC GATGAATACA CGGGATCCGG
1751  GAATAGTGCC AGCACCCCAA AACGAAACAA AGAAAAGACA ACATTAACAA
1801  ACACAACTCT TGAGAGTATA CTAAAAAAAG GTACCTTTGT TAACATCACT
1851  GCTAATCAAC GCATCTATGT CAATAGCTCC ATTAATTTAT CCAATGGCAG
1901  CTTAACTCTT TGGAGTGAGG GTCGGAGCGG TGGCGGCGTT GAGATTAACA
1951  ACGATATTAC CACCGGTGAT GATACCAGAG GTGCAAACTT AACAATTTAC
2001  TCAGGCGGCT GGGTTGATGT TCATAAAAAT ATCTCACTCG GGGCGCAAGG
2051  TAACATAAAC ATTACAGCTA AACAAGATAT CGCCTTTGAG AAAGGAAGCA
2101  ACCAAGTCAT TACAGGTCAA GGGACTATTA CCTCAGGCAA TCAAAAAGGT
2151  TTTAGATTTA ATAATGTCTC TCTAAACGGC ACTGGCAGCG GACTGCAATT
2201  CACCACTAAA AGAACCAATA AATACGCTAT CACAAATAAA TTTGAAGGGA
2251  CTTTAAATAT TTCAGGGAAA GTGAACATCT CAATGGTTTT ACCTAAAAAT
2301  GAAAGTGGAT ATGATAAATT CAAAGGACGC ACTTACTGGA ATTTAACCTC
2351  GAAAGTGGAT ATGATAAATT CAAAGGACGC CCTCACTATT GACTCCAGAG
2401  GAAGCGATAG TGCAGGCACA CTTACCCAGC CTTATAATTT AAACGGTATA
2451  TCATTCAACA AAGACACTAC CTTTAATGTT GAACGAAATG CAAGAGTCAA
```


EP 0 855 446 A1

FIG. 6D.

2501	CTTTGACATC	AAGGCACCAA	TAGGGATAAA	TAAGTATTCT	AGTTTGAATT
2551	ACGCATCATT	TAATGGAAAC	ATTTCAGTTT	CGGGAGGGGG	GAGTGTTGAT
2601	TTCACACTTC	TCGCCTCATC	CTCTAACGTC	CAAACCCCCG	GTGTAGTTAT
2651	AAATTCTAAA	TACTTTAATG	TTTCAACAGG	GTCAAGTTTA	AGATTTAAAA
2701	CTTCAGGCTC	AACAAAAACT	GGCTTCTCAA	TAGAGAAAGA	TTTAACTTTA
2751	AATGCCACCG	GAGGCAACAT	AACACTTTTG	CAAGTTGAAG	GCACCGATGG
2801	AATGATTGGT	AAAGGCATTG	TAGCCAAAAA	AAACATAACC	TTTGAAGGAG
2851	GTAAGATGAG	GTTTGGCTCC	AGGAAAGCCG	TAACAGAAAT	CGAAGGCAAT
2901	GTTACTATCA	ATAACAACGC	TAACGTCACT	CTTATCGGTT	CGGATTTTGA
2951	CAACCATCAA	AAACCTTTAA	CTATTAAAAA	AGATGTCATC	ATTAATAGCG
3001	GCAACCTTAC	CGCTGGAGGC	AATATTGTCA	ATATAGCCGG	AAATCTTACC
3051	GTTGAAAGTA	ACGCTAATTT	CAAAGCTATC	ACAAATTTCA	CTTTTAATGT
3101	AGGCGGCTTG	TTTGACAACA	AAGGCAATTC	AAATATTTCC	ATTGCCAAAG
3151	GAGGGGCTCG	CTTTAAAGAC	ATTGATAATT	CCAAGAATTT	AAGCATCACC
3201	ACCAACTCCA	GCTCCACTTA	CCGCACTATT	ATAAGCGGCA	ATATAACCAA
3251	TAAAAACGGT	GATTTAAATA	TTACGAACGA	AGGTAGTGAT	ACTGAAATGC

FIG.6E.

```
3301  AAATTGGCGG CGATGTCTCG CAAAAAGAAG GTAATCTCAC GATTTCTTCT
3351  GACAAAATCA ATATTACCAA ACAGATAACA ATCAAGGCAG GTGTTGATGG
3401  GGAGAATTCC GATTCAGACG CGACAAACAA TGCCAATCTA ACCATTAAAA
3451  CCAAAGAATT GAAATTAACG CAAGACCTAA ATATTTCAGG TTTCAATAAA
3501  GCAGAGATTA CAGCTAAAGA TGGTAGTGAT TTAACTATTG GTAACACCAA
3551  TAGTGCTGAT GGTACTAATG CCAAAAAAGT AACCTTTAAC CAGGTTAAAG
3601  ATTCAAAAAT CTCTGCTGAC GGTCACAAGG TGACACTACA CAGCAAAGTG
3651  GAAACATCCG GTAGTAATAA CAACACTGAA GATAGCAGTG ACAATAATGC
3701  CGGCTTAACT ATCGATGCAA AAAATGTAAC AGTAAACAAC AATATTACTT
3751  CTCACAAAGC AGTGAGCATC TCTGCGACAA GTGGAGAAAT TACCACTAAA
3801  ACAGGTACAA CCATTAACGC AACCACTGGT AACGTGGAGA TAACCGCTCA
3851  AACAGGTAGT ATCCTAGGTG GAATTGAGTC CAGCTCTGGC TCTGTAACAC
3901  TTACTGCAAC CGAGGGCGCT CTTGCTGTAA GCAATATTTC GGGCAACACC
3951  GTTACTGTTA CTGCAAATAG CGGTGCATTA ACCACTTTGG CAGGCTCTAC
4001  AATTAAAGGA ACCGAGAGTG TAACCACTTC AAGTCAATCA GGCGATATCG
4051  GCGGTACGAT TTCTGGTGGC ACAGTAGAGG TTAAAGCAAC CGAAAGTTTA
```


20050056054

FIG.6F.

```
4101  ACCACTCAAT CCAATTCAAA AATTAAAGCA ACAACAGGCG AGGCTAACGT
4151  AACAAGTGCA ACAGGTACAA TTGGTGGTAC GATTTCCGGT AATACGGTAA
4201  ATGTTACGGC AAACGCTGGC GATTTAACAG TTGGGAATGG CGCAGAAATT
4251  AATGCGACAG AAGGAGCTGC AACCTTAACT ACATCATCGG GCAAATTAAC
4301  TACCGAAGCT AGTTCACACA TTACTTCAGC CAAGGGTCAG GTAAATCTTT
4351  CAGCTCAGGA TGGTAGCGTT GCAGGAAGTA TTAATGCCGC CAATGTGACA
4401  CTAAATACTA CAGGCACTTT AACTACCGTG AAGGGTTCAA ACATTAATGC
4451  AACCAGCGGT ACCTTGGTTA TTAACGCAAA AGACGCTGAG CTAAATGGCG
4501  CAGCATTGGG TAACCACACA GTGGTAAATG CAACCAACGC AAATGGCTCC
4551  GGCAGCGTAA TCGCGACAAC CTCAAGCAGA GTGAACATCA CTGGGGATTT
4601  AATCACAATA AATGGATTAA ATATCATTTC AAAAAACGGT ATAAACACCG
4651  TACTGTTAAA AGGCGTTAAA ATTGATGTGA AATACATTCA ACCGGGTATA
4701  GCAAGCGTAG ATGAAGTAAT TGAAGCGAAA CGCATCCTTG AGAAGGTAAA
4751  AGATTTATCT GATGAAGAAA GAGAAGCGTT AGCTAAACTT GGCGTAAGTG
4801  CTGTACGTTT TATTGAGCCA AATAATACAA TTACAGTCGA TACACAAAAT
4851  GAATTTGCAA CCAGACCATT AAGTCGAATA GTGATTTCTG AAGGCAGGGC
4901  GTGTTTCTCA AACAGTGATG GCGCGACGGT GTGCGTTAAT ATCGCTGATA
```


SUBSTITUTE SHEET (RULE 26)

FIG.6G.

```
4951  ACGGGCGGTA GCGGTCAGTA ATTGACAAGG TAGATTTCAT CCTGCAATGA
5001  AGTCATTTTA TTTTCGTATT ATTTACTGTG TGGGTTAAAG TTCAGTACGG
5051  GCTTTACCCA TCTTGTAAAA AATTACGGAG AATACAATAA AGTATTTTTA
5101  ACAGGTTATT ATTATGAAAA ATATAAAAAG CAGATTAAAA CTCAGTGCAA
5151  TATCAGTATT GCTTGGCCTG GCTTCTTCAT CATTGTATGC AGAAGAAGCG
5201  TTTTTAGTAA AAGGCTTTCA GTTATCTGGT GCACTTGAAA CTTTAAGTGA
5251  AGACGCCCAA CTGTCTGTAG CAAAATCTTT ATCTAAATAC CAAGGCTCGC
5301  AAACTTTAAC AAACCTAAAA ACAGCACAGC TTGAATTACA GGCTGTGCTA
5351  GATAAGATTG AGCCAAATAA GTTTGATGTG ATATTGCCAC AACAAACCAT
5401  TACGGATGGC AATATTATGT TTGAGCTAGT CTCGAAATCA GCCGCAGAAA
5451  GCCAAGTTTT TTATAAGGCG AGCCAGGGTT ATAGTGAAGA AAATATCGCT
5501  CGTAGCCTGC CATCTTTGAA ACAAGGAAAA GTGTATGAAG ATGGTCGTCA
5551  GTGGTTCGAT TTGCGTGAAT TCAATATGGC AAAAGAAAAT CCACTTAAAG
5601  TCACTCGCGT GCATTACGAG TTAAACCCTA AAAACAAAAC CTCTGATTTG
5651  GTAGTTGCAG GTTTTTCGCC TTTTGGCAAA ACGCGTAGCT TTGTTTCCTA
5701  TGATAATTTC GGCGCAAGGG AGTTTAACTA TCAACGTGTA AGTCTAGGTT
```


SUBSTITUTE SHEET (RULE 26)

FIG.6H.

```
5751  TTGTAAATGC CAATTTGACC GGACATGATG ATGTATTAAA TCTAAACGCA
5801  TTGACCAATG TAAAAGCACC ATCAAAATCT TATGCGGTAG GCATAGGATA
5851  TACTTATCCG TTTTATGATA AACACCAATC CTTAAGTCTT TATACCAGCA
5901  TGAGTTATGC TGATTCTAAT GATATCGACG GCTTACCAAG TGCGATTAAT
5951  CGTAAATTAT CAAAAGGTCA ATCTATCTCT GCGAATCTGA AATGGAGTTA
6001  TTATCTCCCG ACATTTAACC TTGGAATGGA AGACCAGTTT AAAATTAATT
6051  TAGGCTACAA CTACCGCCAT ATTAATCAAA CATCCGAGTT AAACACCCTG
6101  GGTGCAACGA AGAAAAAATT TGCAGTATCA GGCGTAAGTG CAGGCATTGA
6151  TGGACATATC CAATTTACCC CTAAAACAAT CTTTAATATT GATTTAACTC
6201  ATCATTATTA CGCGAGTAAA TTACCAGGCT CTTTTGGAAT GGAGCGCATT
6251  GGCGAAACAT TTAATCGCAG CTATCACATT AGCACAGCCA GTTTAGGGTT
6301  GAGTCAAGAG TTTGCTCAAG GTTGGCATTT TAGCAGTCAA TTATCGGGTC
6351  AGTTTACTCT ACAAGATATA AGTAGCATAG ATTTATTCTC TGTAACAGGT
6401  ACTTATGGCG TCAGAGGCTT TAAATACGGC GGTGCAAGTG GTGAGCGCGG
6451  TCTTGTATGG CGTAATGAAT TAAGTATGCC AAAATACACC CGCTTTCAAA
6501  TCAGCCCTTA TGCGTTTTAT GATGCAGGTC AGTTCCGTTA TAATAGCGAA
6551  AATGCTAAAA CTTACGGCGA AGATATGCAC ACGGTATCCT CTGCGGGTTT
```


WO 00/22820 PCT/US99/24076

10092880.030802

FIG.6I.

```
6601  AGGCATTAAA ACCTCTCCTA CACAAAACTT AAGCTTAGAT GCTTTTGTTG
6651  CTCGTCGCTT TGCAAATGCC AATAGTGACA ATTTGAATGG CAACAAAAAA
6701  CGCACAAGCT CACCTACAAC CTTCTGGGGT AGATTAACAT TCAGTTTCTA
6751  ACCCTGAAAT TTAATCAACT GGTAAGCGTT CCGCCTACCA GTTTATAACT
6801  ATATGCTTTA CCCGCCAATT TACAGTCTAT ACGCAACCCT GTTTTCATCC
6851  TTATATATCA AACAAACTAA GCAAACCAAG CAAACCAAGC AAACCAAGCA
6901  AACCAAGCAA ACCAAGCAAA CCAAGCAAAC CAAGCAAACC AAGCAAACCA
6951  AGCAAACCAA GCAAACCAAG CAAACCAAGC AAACCAAGCA ATGCTAAAAA
7001  ACAATTTATA TGATAAACTA AAACATACTC CATACCATGG CAATACAAGG
7051  GATTTAATAA TATGACAAAA GAAAATTTAC AAAGTGTTCC ACAAAATACG
7101  ACCGCTTCAC TTGTAGAATC AAACAACGAC CAAACTTCCC TGCAAATACT
7151  TAAACAACCA CCCAAACCCA ACCTATTACG CCTGGAACAA CATGTCGCCA
7201  AAAAAGATTA TGAGCTTGCT TGCCGCGAAT TAATGGCGAT TTTGGAAAAA
7251  ATGGACGCTA ATTTTGGAGG CGTTCACGAT ATTGAATTTG ACGCACCTGC
7301  TCAGCTGGCA TATCTACCCG AAAAACTACT AATTCATTTT GCCACTCGTC
7351  TCGCTAATGC AATTACAACA CTCTTTTCCG ACCCCGAATT GGCAATTTCC
```

FIG.6J.

```
7401  GAAGAAGGGG CATTAAAGAT GATTAGCCTG CAACGCTGGT TGACGCTGAT
7451  TTTTGCCTCT TCCCCCTACG TTAACGCAGA CCATATTCTC AATAAATATA
7501  ATATCAACCC AGATTCCGAA GGTGGCTTTC ATTTAGCAAC AGACAACTCT
7551  TCTATTGCTA AATTCTGTAT TTTTTACTTA CCCGAATCCA ATGTCAATAT
7601  GAGTTTAGAT GCGTTATGGG CAGGGAATCA ACAACTTTGT GCTTCATTGT
7651  GTTTTGCGTT GCAGTCTTCA CGTTTTATTG GTACTGCATC TGCGTTTCAT
7701  AAAAGAGCGG TGGTTTTACA GTGGTTTCCT AAAAAACTCG CCGAAATTGC
7751  TAATTTAGAT GAATTGCCTG CAAATATCCT TCATGATGTA TATATGCACT
7801  GCAGTTATGA TTTAGCAAAA AACAAGCACG ATGTTAAGCG TCCATTAAAC
7851  GAACTTGTCC GCAAGCATAT CCTCACGCAA GGATGGCAAG ACCGCTACCT
7901  TTACACCTTA GGTAAAAAGG ACGGCAAACC TGTGATGATG GTACTGCTTG
7951  AACATTTTAA TTCGGGACAT TCGATTTATC GCACGCATTC AACTTCAATG
8001  ATTGCTGCTC GAGAAAAATT CTATTTAGTC GGCTTAGGCC ATGAGGGCGT
8051  TGATAACATA GGTCGAGAAG TGTTTGACGA GTTCTTTGAA ATCAGTAGCA
8101  ATAATATAAT GGAGAGACTG TTTTTTATCC GTAAACAGTG CGAAACTTTC
8151  CAACCCGCAG TGTTCTATAT GCCAAGCATT GGCATGGATA TTACCACGAT
```


WO 99/55850 PCT/US99/09507

FIG.6K.

```
8201  TTTTGTGAGC AACACTCGGC TTGCCCCTAT TCAAGCTGTA GCCTTGGGTC
8251  ATCCTGCCAC TACGCATTCT GAATTTATTG ATTATGTCAT CGTAGAAGAT
8301  GATTATGTGG GCAGTGAAGA TTGTTTAGC  GAAACCCTTT TACGCTTACC
8351  CAAAGATGCC CTACCTTATG TACCATCTGC ACTCGCCCCA CAAAAAGTGG
8401  ATTATGTACT CAGGGAAAAC CCTGAAGTAG TCAATATCGG TATTGCCGCT
8451  ACCACAATGA AATTAAACCC TGAATTTTTG CTAACATTGC AAGAAATCAG
8501  AGATAAAGCT AAAGTCAAAA TACATTTTCA TTTCGCACTT GGACAATCAA
8551  CAGGCTTGAC ACACCCTTAT GTCAAATGGT TTATCGAAAG CTATTTAGGT
8601  GACGATGCCA CTGCACATCC CCACGCACCT TATCACGATT ATCTGGCAAT
8651  ATTGCGTGAT TGCGATATGC TACTAAATCC GTTTCCTTTC GGTAATACTA
8701  ACGGCATAAT TGATATGGTT ACATTAGGTT TAGTTGGTGT ATGCAAAACG
8751  GGGGATGAAG TACATGAACA TATTGATGAA GGTCTGTTTA AACGCTTAGG
8801  ACTACCAGAA TGGCTGATAG CCGACACACG AGAAACATAT ATTGAATGTG
8851  CTTTGCGTCT AGCAGAAAAC CATCAAGAAC GCCTTGAACT CCGTCGTTAC
8901  ATCATAGAAA ACAACGGCTT ACAAAAGCTT TTTACAGGCG ACCCTCGTCC
8951  ATTGGGCAAA ATACTGCTTA AGAAAACAAA TGAATGGAAG CGGAAGCACT
9001  TGAGTAAAAA ATAACGGTTT TTTAAAGTAA AAGTGCGGTT AATTTTCAAA
```


WO 00/55350 PCT/US00/05501

10092880.030802

FIG.6L.

9051 GCGTTTTAAA AACCTCTCAA AAATCAACCG CACTTTTATC TTTATAACGC
9101 TCCCGCGCGC TGACAGTTTA TCTCTTTCTT AAAATACCCA TAAAATTGTG
9151 GCAATAGTTG GGTAATCAAA TTCAATTGTT GATACGGCAA ACTAAAGACG
9201 GCGCGTTCTT CGGCAGTCAT C

FIG.7A.

```
  1 CGCCACTTCA ATTTTGGATT GTTGAAATTC AACTAACCAA AAAGTGCGGT
 51 TAAAATCTGT GGAGAAAATA GGTTGTAGTG AAGAACGAGG TAATTGTTCA
101 AAAGGATAAA GCTCTCTTAA TTGGGCATTG GTTGGCGTTT CTTTTTCGGT
151 TAATAGTAAA TTATATTCTG GACGACTATG CAATCCACCA ACAACTTTAC
201 CGTTGGTTTT AAGCGTTAAT GTAAGTTCTT GCTCTTCTTG GCGAATACGT
251 AATCCCATTT TTTGTTTAGC AAGAAAATGA TCGGGATAAT CATAATAGGT
301 GTTGCCCAAA AATAAATTTT GATGTTCTAA AATCATAAAT TTTGCAAGAT
351 ATTGTGGCAA TTCAATACCT ATTTGTGGCG AAATCGCCAA TTTTAATTCA
401 ATTTCTTGTA GCATAATATT TCCCACTCAA ATCAACTGGT TAAATATACA
451 AGATAATAAA AATAAATCAA GATTTTTGTG ATGACAAACA ACAATTACAA
501 CACCTTTTTT GCAGTCTATA TGCAAATATT TTAAAAAAAT AGTATAAATC
551 CGCCATATAA AATGGTATAA TCTTTCATCT TTCATCTTTC ATCTTTCATC
601 TTTCATCTTT CATCTTTCAT CTTTCATCTT TCATCTTTCA TCTTTCATCT
651 TTCATCTTTC ATCTTTCATC TTTCATCTTT CACATGAAAT GATGAACCGA
701 GGGAAGGGAG GGAGGGGCAA GAATGAAGAG GGAGCTGAAC GAACGCAAAT
751 GATAAAGTAA TTTAATTGTT CAACTAACCT TAGGAGAAAA TATGAACAAG
```

10092880 .030802

FIG.7B.

```
801   ATATATCGTC TCAAATTCAG CAAACGCCTG AATGCTTTGG TTGCTGTGTC
851   TGAATTGGCA CGGGGTTGTG ACCATTCCAC AGAAAAAGGC AGCGAAAAAC
901   CTGCTCGCAT GAAAGTGCGT CACTTAGCGT TAAAGCCACT TTCCGCTATG
951   TTACTATCTT TAGGTGTAAC ATCTATTCCA CAATCTGTTT TAGCAAGCGG
1001  CAATTTAACA TCGACCAAAA TGAAATGGTG CAGTTTTTAC AAGAAAACAA
1051  GTAATAAAAC CATTATCCGC AACAGTGTTG ACGCTATCAT TAATTGGAAA
1101  CAATTTAACA TCGACCAAAA TGAAATGGTG CAGTTTTTAC AAGAAAACAA
1151  CAACTCCGCC GTATTCAACC GTGTTACATC TAACCAAATC TCCCAATTAA
1201  AAGGGATTTT AGATTCTAAC GGACAAGTCT TTTTAATCAA CCCAAATGGT
1251  ATCACAATAG GTAAAGACGC AATTATTAAC ACTAATGGCT TTACGGCTTC
1301  TACGCTAGAC ATTTCTAACG AAAACATCAA GGCGCGTAAT TTCACCTTCG
1351  AGCAAACCAA AGATAAAGCG CTCGCTGAAA TTGTGAATCA CGGTTTAATT
1401  ACTGTCGGTA AAGACGGCAG TGTAAATCTT ATTGGTGGCA AAGTGAAAAA
1451  CGAGGGTGTG ATTAGCGTAA ATGGTGGCAG CATTTCTTTA CTCGCAGGGC
1501  AAAAAATCAC CATCAGCGAT ATAATAAACC CAACCATTAC TTACAGCATT
1551  GCCGCGCCTG AAAATGAAGC GGTCAATCTG GGCGATATTT TTGCCAAAGG
```

FIG.7C.

1601	CGGTAACATT	AATGTCCGTG	CTGCCACTAT	TCGAAACCAA	GGTAAACTTT
1651	CTGCTGATTC	TGTAAGCAAA	GATAAAAGCG	GCAATATTGT	TCTTTCCGCC
1701	AAAGAGGGTG	AAGCGGAAAT	TGGCGGTGTA	ATTTCCGCTC	AAAATCAGCA
1751	AGCTAAAGGC	GGCAAGCTGA	TGATTACAGG	CGATAAAGTC	ACATTAAAAA
1801	CAGGTGCAGT	TATCGACCTT	TCAGGTAAAG	AAGGGGGAGA	AACTTACCTT
1851	GGCGGTGACG	AGCGCGGCGA	AGGTAAAAAC	GGCATTCAAT	TAGCAAAGAA
1901	AACCTCTTTA	GAAAAAGGCT	CAACCATCAA	TGTATCAGGC	AAAGAAAAAG
1951	GCGGACGCGC	TATTGTGTGG	GGCGATATTG	CGTTAATTGA	CGGCAATATT
2001	AACGCTCAAG	GTAGTGGTGA	TATCGCTAAA	ACCGGTGGTT	TTGTGGAGAC
2051	ATCGGGGCAT	TATTTATCCA	TTGACAGCAA	TGCAATTGTT	AAAACAAAAG
2101	AGTGGTTGCT	AGACCCTGAT	GATGTAACAA	TTGAAGCCGA	AGACCCCCTT
2151	CGCAATAATA	CCGGTATAAA	TGATGAATTC	CCAACAGGCA	CCGGTGAAGC
2201	AAGCGACCCT	AAAAAAAATA	GCGAACTCAA	AACAACGCTA	ACCAATACAA
2251	CTATTTCAAA	TTATCTGAAA	AACGCCTGGA	CAATGAATAT	AACGGCATCA
2301	AGAAAACTTA	CCGTTAATAG	CTCAATCAAC	ATCGGAAGCA	ACTCCCACTT
2351	AATTCTCCAT	AGTAAAGGTC	AGCGTGGCGG	AGGCGTTCAG	ATTGATGGAG
2401	ATATTACTTC	TAAAGGCGGA	AATTTAACCA	TTTATTCTGG	CGGATGGGTT

10092880.030802

10092380.030802

FIG.7D.

2451	GATGTTCATA	AAAATATTAC	GCTTGATCAG	GGTTTTTTAA	ATATTACCGC
2501	CGCTTCCGTA	GCTTTTGAAG	GTGGAAATAA	CAAAGCACGC	GACGCGGCAA
2551	ATGCTAAAAT	TGTCGCCCAG	GGCACTGTAA	CCATTACAGG	AGAGGGAAAA
2601	GATTTCAGGG	CTAACAACGT	ATCTTTAAAC	GGAACGGGTA	AAGGTCTGAA
2651	TATCATTTCA	TCAGTGAATA	ATTTAACCCA	CAATCTTAGT	GGCACAATTA
2701	ACATATCTGG	GAATATAACA	ATTAACCAAA	CTACGAGAAA	GAACACCTCG
2751	TATTGGCAAA	CCAGCCATGA	TTCGCACTGG	AACGTCAGTG	CTCTTAATCT
2801	AGAGACAGGC	GCAAATTTTA	CCTTTATTAA	ATACATTTCA	AGCAATAGCA
2851	AAGGCTTAAC	AACACAGTAT	AGAAGCTCTG	CAGGGGTGAA	TTTTAACGGC
2901	GTAAATGGCA	ACATGTCATT	CAATCTCAAA	GAAGGAGCGA	AAGTTAATTT
2951	CAAATTAAAA	CCAAACGAGA	ACATGAACAC	AAGCAAACCT	TTACCAATTC
3001	GGTTTTTAGC	CAATATCACA	GCCACTGGTG	GGGGCTCTGT	TTTTTTTGAT
3051	ATATATGCCA	ACCATTCTGG	CAGAGGGGCT	GAGTTAAAAA	TGAGTGAAAT
3101	TAATATCTCT	AACGGCGCTA	ATTTTACCTT	AAATTCCCAT	GTTCGCGGCG
3151	ATGACGCTTT	TAAAATCAAC	AAAGACTTAA	CCATAAATGC	AACCAATTCA
3201	AATTTCAGCC	TCAGACAGAC	GAAAGATGAT	TTTTATGACG	GGTACGCACG

FIG.7E.

```
3251  CAATGCCATC AATTCAACCT ACAACATATC CATTCTGGGC GGTAATGTCA
3301  CCCTTGGTGG ACAAAACTCA AGCAGCAGCA TTACGGGGAA TATTACTATC
3351  GAGAAAGCAG CAAATGTTAC GCTAGAAGCC AATAACGCCC CTAATCAGCA
3401  AAACATAAGG GATAGAGTTA TAAAACTTGG CAGCTTGCTC GTTAATGGGA
3451  GTTTAAGTTT AACTGGCGAA AATGCAGATA TTAAAGGCAA TCTCACTATT
3501  TCAGAAAGCG CCACTTTTAA AGGAAAGACT AGAGATACCC TAAATATCAC
3551  CGGCAATTTT ACCAATAATG GCACTGCCGA AATTAATATA ACACAAGGAG
3601  TGGTAAAACT TGGCAATGTT ACCAATGATG GTGATTTAAA CATTACCACT
3651  CACGCTAAAC GCAACCAAAG AAGCATCATC GGCGGAGATA TAATCAACAA
3701  AAAAGGAAGC TTAAATATTA CAGACAGTAA TAATGATGCT GAAATCCAAA
3751  TTGGCGGCAA TATCTCGCAA AAAGAAGGCA ACCTCACGAT TTCTTCCGAT
3801  AAAATTAATA TCACCAAACA GATAACAATC AAAAAGGGTA TTGATGGAGA
3851  GGACTCTAGT TCAGATGCGA CAAGTAATGC CAACCTAACT ATTAAAACCA
3901  AAGAATTGAA ATTGACAGAA GACCTAAGTA TTTCAGGTTT CAATAAAGCA
3951  GAGATTACAG CCAAAGATGG TAGAGATTTA ACTATTGGCA ACAGTAATGA
4001  CGGTAACAGC GGTGCCGAAG CCAAAACAGT AACTTTTAAC AATGTTAAAG
```


WO 99/53050 PCT/US99/07905

10092880.030802

FIG.7F.

4051	ATTCAAAAAT	CTCTGCTGAC	GGTCACAATG	TGACACTAAA	TAGCAAAGTG
4101	AAAACATCTA	GCAGCAATGG	CGGACGTGAA	AGCAATAGCG	ACAACGATAC
4151	CGGCTTAACT	ATTACTGCAA	AAAATGTAGA	AGTAAACAAA	GATATTACTT
4201	CTCTCAAAAC	AGTAAATATC	ACCGCGTCGG	AAAAGGTTAC	CACCACAGCA
4251	GGCTCGACCA	TTAACGCAAC	AAATGGCAAA	GCAAGTATTA	CAACCAAAAC
4301	AGGTGATATC	AGCGGTACGA	TTTCCGGTAA	CACGGTAAGT	GTTAGCGCGA
4351	CTGGTGATTT	AACCACTAAA	TCCGGCTCAA	AAATTGAAGC	GAAATCGGGT
4401	GAGGCTAATG	TAACAAGTGC	AACAGGTACA	ATTGGCGGTA	CAATTTCCGG
4451	TAATACGGTA	AATGTTACGG	CAAACGCTGG	CGATTTAACA	GTTGGGAATG
4501	GCGCAGAAAT	TAATGCGACA	GAAGGAGCTG	CAACCTTAAC	CGCAACAGGG
4551	AATACCTTGA	CTACTGAAGC	CGGTTCTAGC	ATCACTTCAA	CTAAGGGTCA
4601	GGTAGACCTC	TTGGCTCAGA	ATGGTAGCAT	CGCAGGAAGC	ATTAATGCTG
4651	CTAATGTGAC	ATTAAATACT	ACAGGCACCT	TAACCACCGT	GGCAGGCTCG
4701	GATATTAAAG	CAACCAGCGG	CACCTTGGTT	ATTAACGCAA	AAGATGCTAA
4751	GCTAAATGGT	GATGCATCAG	GTGATAGTAC	AGAAGTGAAT	GCAGTCAACG
4801	ACTGGGGATT	TGGTAGTGTG	ACTGCGGCAA	CCTCAAGCAG	TGTGAATATC
4851	ACTGGGGATT	TAAACACAGT	AAATGGGTTA	AATATCATTT	CGAAAGATGG

10092880.030802

FIG.7G.

4901 TAGAAACACT GTGCGCTTAA GAGGCAAGGA AATTGAGGTG AAATATATCC
4951 AGCCAGGTGT AGCAAGTGTA GAAGAAGTAA TTGAAGCGAA ACGCGTCCTT
5001 GAAAAAGTAA AAGATTTATC TGATGAAGAA AGAGAAACAT TAGCTAAACT
5051 TGGTGTAAGT GCTGTACGTT TTGTTGAGCC AAATAATACA ATTACAGTCA
5101 ATACACAAAA TGAATTTACA ACCAGACCGT CAAGTCAAGT GATAATTTCT
5151 GAAGGTAAGG CGTGTTTCTC AAGTGGTAAT GGCGCACGAG TATGTACCAA
5201 TGTTGCTGAC GATGGACAGC CGTAGTCAGT AATTGACAAG GTAGATTTCA
5251 TCCTGCAATG AAGTCATTTT ATTTTCGTAT TATTTACTGT GTGGGTTAAA
5301 GTTCAGTACG GGCTTTACCC ATCTTGTAAA AAATTACGGA GAATACAATA
5351 AAGTATTTTT AACAGGTTAT TATTATGAAA AATATAAAAA GCAGATTAAA
5401 ACTCAGTGCA ATATCAGTAT TGCTTGGCCT GGCTTCTTCA TCATTGTATG
5451 CAGAAGAAGC GTTTTTAGTA AAAGGCTTTC AGTTATCTGG TGCACTTGAA
5501 ACTTTAAGTG AAGACGCCCA ACTGTCTGTA GCAAAATCTT TATCTAAATA
5551 CCAAGGCTCG CAAACTTTAA CAAACCTAAA AACAGCACAG CTTGAATTAC
5601 AGGCTGTGCT AGATAAGATT GAGCCAAATA AATTTGATGT GATATTGCCG
5651 CAACAAACCA TTACGGATGG CAATATCATG TTTGAGCTAG TCTCGAAATC

FIG. 7H.

5701 AGCCGCAGAA AGCCAAGTTT TTTATAAGGC GAGCCAGGGT TATAGTGAAG
5751 AAAATATCGC TCGTAGCCTG CCATCTTTGA AACAAGGAAA AGTGTATGAA
5801 GATGGTCGTC AGTGGTTCGA TTTGCGTGAA TTTAATATGG CAAAAGAAAA
5851 CCCGCTTAAG GTTACCCGTG TACATTACGA ACTAAACCCT AAAAACAAAA
5901 CCTCTAATTT GATAATTGCG GGCTTCTCGC CTTTTGGTAA AACGCGTAGC
5951 TTTATTTCTT ATGATAATTT CGGCGCGAGA GAGTTTAACT ACCAACGTGT
6001 AAGCTTGGGT TTTGTTAATG CCAATTTAAC TGGTCATGAT GATGTGTTAA
6151 TTATACCAGT ATGAGTTATG CTGATTCTAA TGATATCGAC GGCTTACCAA
6201 GTGCGATTAA TCGTAAATTA TCAAAAGGTC AATCTATCTC TGCGAATCTG
6251 AAATGGAGTT ATTATCTCCC AACATTTAAC CTTGGCATGG AAGACCAATT
6301 TAAAATTAAT TTAGGCTACA ACTACCGCCA TATTAATCAA ACCTCCGCGT
6351 TAAATCGCTT GGGTGAAACG AAGAAAAAAT TTGCAGTATC AGGCGTAAGT
6401 GCAGGCATTG ATGGACATAT CCAATTTACC CCTAAAACAA TCTTTAATAT
6451 TGATTTAACT CATCATTATT ACGCGAGTAA ATTACCAGGC TCTTTTGGAA
6501 TGGAGCGCAT TGGCGAAACA TTTAATCGCA GCTATCACAT TAGCACAGCC
6551 AGTTTAGGGT TGAGTCAAGA GTTTGCTCAA GGTTGGCATT TTAGCAGTCA
6601 ATTATCAGGT CAATTTACTC TACAAGATAT TAGCAGTATA GATTTATTCT

10092380.030802

FIG.7I.

6651	CTGTAACAGG	TACTTATGGC	GTCAGAGGCT	TTAAATACGG	CGGTGCAAGT
6701	GGTGAGCGCG	GTCTTGTATG	GCGTAATGAA	TTAAGTATGC	CAAAATACAC
6751	CCGCTTCCAA	ATCAGCCCTT	ATGCGTTTTA	TGATGCAGGT	CAGTTCCGTT
6801	ATAATAGCGA	AAATGCTAAA	ACTTACGGCG	AAGATATGCA	CACGGTATCC
6851	TCTGCGGGTT	TAGGCATTAA	AACCTCTCCT	ACACAAAACT	TAAGCCTAGA
6901	TGCTTTTGTT	GCTCGTCGCT	TTGCAAATGC	CAATAGTGAC	AATTTGAATG
6951	GCAACAAAAA	ACGCACAAGC	TCACCTACAA	CCTTCTGGGG	GAGATTAACA
7001	TTCAGTTTCT	AACCCTGAAA	TTTAATCAAC	TGGTAAGCGT	TCCGCCTACC
7051	AGTTTATAAC	TATATGCTTT	ACCCGCCAAT	TTACAGTCTA	TAGGCAACCC
7101	TGTTTTTACC	CTTATATATC	AAATAAACAA	GCTAAGCTGA	GCTAAGCAAA
7151	CCAAGCAAAC	TCAAGCAAGC	CAAGTAATAC	TAAAAAAACA	ATTTATATGA
7201	TAAACTAAAG	TATACTCCAT	GCCATGGCGA	TACAAGGGAT	TTAATAATAT
7251	GACAAAAGAA	AATTTGCAAA	ACGCTCCTCA	AGATGCGACC	GCTTTACTTG
7301	CGGAATTAAG	CAACAATCAA	ACTCCCCTGC	GAATATTTAA	ACAACCACGC
7351	AAGCCCAGCC	TATTACGCTT	GGAACAACAT	ATCGCAAAAA	AAGATTATGA
7401	GTTTGCTTGT	CGTGAATTAA	TGGTGATTCT	GGAAAAAATG	GACGCTAATT

FIG.7J.

```
7451  TTGGAGGCGT TCACGATATT GAATTTGACG CACCCGCTCA GCTGGCATAT
7501  CTACCCGAAA AATTACTAAT TTATTTTGCC ACTCGTCTCG CTAATGCAAT
7551  TACAACACTC TTTTCCGACC CCGAATTGGC AATTTCTGAA GAAGGGGCGT
7601  TAAAGATGAT TAGCCTGCAA CGCTGGTTGA CGCTGATTTT TGCCTCTTCC
7651  CCCTACGTTA ACGCAGACCA TATTCTCAAT AAATATAATA TCAACCCAGA
7701  TTCCGAAGGT GGCTTTCATT TAGCAACAGA CAACTCTTCT ATTGCTAAAT
7751  TCTGTATTTT TTACTTACCC GAATCCAATG TCAATATGAG TTTAGATGCG
7801  TTATGGGCAG GGAATCAACA ACTTTGTGCT TCATTGTGTT TTGCGTTGCA
7851  GTCTTCACGT TTTATTGGTA CCGCATCTGC GTTTCATAAA AGAGCGGTGG
7901  TTTTACAGTG GTTTCCTAAA AAACTCGCCG AAATTGCTAA TTTAGATGAA
7951  TTGCCTGCAA ATATCCTTCA TGATGTATAT ATGCACTGCA GTTATGATTT
8001  AGCAAAAAAC AAGCACGATG TTAAGCGTCC ATTAAACGAA CTTGTCCGCA
8051  AGCATATCCT CACGCAAGGA TGGCAAGACC GCTACCTTTA CACCTTAGGT
8101  AAAAAGGACG GCAAACCTGT GATGATGGTA CTGCTTGAAC ATTTTAATTC
8151  GGGACATTCG ATTTATCGTA CACATTCAAC TTCAATGATT GCTGCTCGAG
8201  AAAAATTCTA TTTAGTCGGC TTAGGCCATG AGGGCGTTGA TAAAATAGGT
```

10092380 .030802

FIG.7K.

8251 CGAGAAGTGT TTGACGAGTT CTTTGAAATC AGTAGCAATA ATATAATGGA
8301 GAGACTGTTT TTTATCCGTA AACAGTGCGA AACTTTCCAA CCCGCAGTGT
8351 TCTATATGCC AAGCATTGGC ATGGATATTA CCACGATTTT TGTGAGCAAC
8401 ACTCGGCTTG CCCCTATTCA AGCTGTAGCC CTGGGTCATC CTGCCACTAC
8451 GCATTCTGAA TTTATTGATT ATGTCATCGT AGAAGATGAT TATGTGGGCA
8501 GTGAAGATTG TTTCAGCGAA ACCCTTTTAC GCTTACCCAA AGATGCCCTA
8551 CCTTATGTAC CTTCTGCACT CGCCCCACAA AAAGTGGATT ATGTACTCAG
8601 GGAAAACCCT GAAGTAGTCA ATATCGGTAT TGCCGCTACC ACAATGAAAT
8651 TAAACCCTGA ATTTTTGCTA ACATTGCAAG AAATCAGAGA TAAAGCTAAA
8701 GTCAAAATAC ATTTTCATTT CGCACTTGGA CAATCAACAG GCTTGACACA
8751 CCCTTATGTC AAATGGTTTA TCGAAAGCTA TTTAGGTGAC GATGCCACTG
8801 CACATCCCCA CGCACCTTAT CACGATTATC TGGCAATATT GCGTGATTGC
8851 GATATGCTAC TAAATCCGTT TCCTTTCGGT AATACTAACG GCATAATTGA
8901 TATGGTTACA TTAGGTTTAG TTGGTGTATG CAAAACGGGG GATGAAGTAC
8951 ATGAACATAT TGATGAAGGT CTGTTTAAAC GCTTAGGACT ACCAGAATGG
9001 CTGATAGCCG ACACACGAGA AACATATATT GAATGTGCTT TGCGTCTAGC
9051 AGAAAACCAT CAAGAACGCC TTGAACTCCG TCGTTACATC ATAGAAAACA

FIG.7L.

9101 ACGGCTTACA AAAGCTTTTT ACAGGCGACC CTCGTCCATT GGGCAAAATA
9151 CTGCTTAAGA AAACAAATGA ATGGAAGCGG AAGCACTTGA GTAAAAAATA
9201 ACGGTTTTTT AAAGTAAAAG TGCGGTTAAT TTTCAAAGCG TTTTAAAAAC
9251 CTCTCAAAAA TCAACCGCAC TTTTATCTTT ATAACGATCC CGCACGCTGA
9301 CAGTTTATCA GCCTCCCGCC ATAAAACTCC GCCTTTCATG GCGGAGATTT
9351 TAGCCAAAAC TGGCAGAAAT TAAAGGCTAA AATCACCAAA TTGCACCACA
9401 AAATCACCAA TACCCACAAA AAA

10092880 .030802

FIG.8A

```
1 ATGAACAAGA TATATCGTCT CAAATTCAGC AAACGCCTGA ATGCTTTGGT
  TGCTGTGTCT GAATTGACAC GGGGTTGTGA CCATTCCACA GAAAAAGGCA
101 GTGAAAAACC TGTTCGTACG AAAGTACGCC ACTTGGCGTT AAAGCCACTT
  TCCGCTATAT TGCTATCTTT GGGCATGGCA TCCATTCCGC AATCTGTTTT
201 AGCGAGCGGT TTACAGGGAA TGAGCGTCGT ACACGGTACA GCAACCATGC
  AAGTAGACGG CAATAAAACC ACTATCCGTA ATAGCGTCAA TGCTATCATC
301 AATTGGAAAC AATTTAACAT TGACCAAAAT GAAATGGTGC AGTTTTTACA
  AGAAAGCAGC AACTCTGCCG TTTTCAACCG TGTTACATCT GACCAAATCT
401 CCCAATTAAA AGGGATTTTA GATTCTAACG GACAAGTCTT TTTAATCAAC
  CCAAATGGTA TCACAATAGG TAAAGACGCA ATTATTAACA CTAATGGCTT
501 TACTGCTTCT ACGCTAGACA TTTCTAACGA AAACATCAAG GCGCGTAATT
  TCACCCTTGA GCAAACCAAG GATAAAGCAC TCGCTGAAAT CGTGAATCAC
601 GGTTTAATTA CCGTTGGTAA AGACGGTAGC GTAAACCTTA TTGGTGGCAA
  AGTGAAAAAC GAGGGCGTGA TTAGCGTAAA TGGCGGTAGT ATTTCTTTAC
701 TTGCAGGGCA AAAAATCACC ATCAGCGATA TAATAAATCC AACCATCACT
  TACAGCATTG CTGCACCTGA AAACGAAGCG ATCAATCTGG GCGATATTTT
```

10092880.030802

10092880.030802

FIG 8B

801 TGCCAAAGGT GGTAACATTA ATGTCCGCGC TGCCACTATT CGCAATAAAG GTAAACTTTC TGCCGACTCT GTAAGCAAAG ATAAAAGTGG TAACATTGTT

901 CTCTCTGCCA AAGAAGGTGA AGCGGAAATT GGCGGTGTAA TTTCCGCTCA AAATCAGCAA GCCAAAGGTG GTAAGTTGAT GATTACAGGC GATAAAGTTA

1001 CATTGAAAAC GGGTGCAGTT ATCGACCTTT CGGGTAAAGA AGGGGGAGAA ACTTATCTTG GCGGTGACGA GCGTGGCGAA GGTAAAAACG GCATTCAATT

1101 AGCAAAGAAA ACCACTTTAG AAAAAGGCTC AACAATTAAT GTGTCAGGTA AAGAAAAAGG TGGGCGCGCT ATTGTATGGG GCGATATTGC GTTAATTGAC

1201 GGCAATATTA ATGCCCAAGG TAAAGATATC GCTAAAACTG GTGGTTTTGT GGAGACGTCG GGGCATTACT TATCCATTGA TGATAACGCA ATTGTTAAAA

1301 CAAAAGAATG GCTACTAGAC CCAGAGAATG TGACTATTGA AGCTCCTTCC GCTTCTCGCG TCGAGCTGGG TGCCGATAGG AATTCCCACT CGGCAGAGGT

1401 GATAAAAGTG ACCCTAAAAA AAAATAACAC CTCCTTGACA ACACTAACCA ATACAACCAT TTCAAATCTT CTGAAAAGTG CCCACGTGGT GAACATAACG

1501 GCAAGGAGAA AACTTACCGT TAATAGCTCT ATCAGTATAG AAAGAGGCTC CCACTTAATT CTCCACAGTG AAGGTCAGGG CGGTCAAGGT GTTCAGATTG

FIG.8C

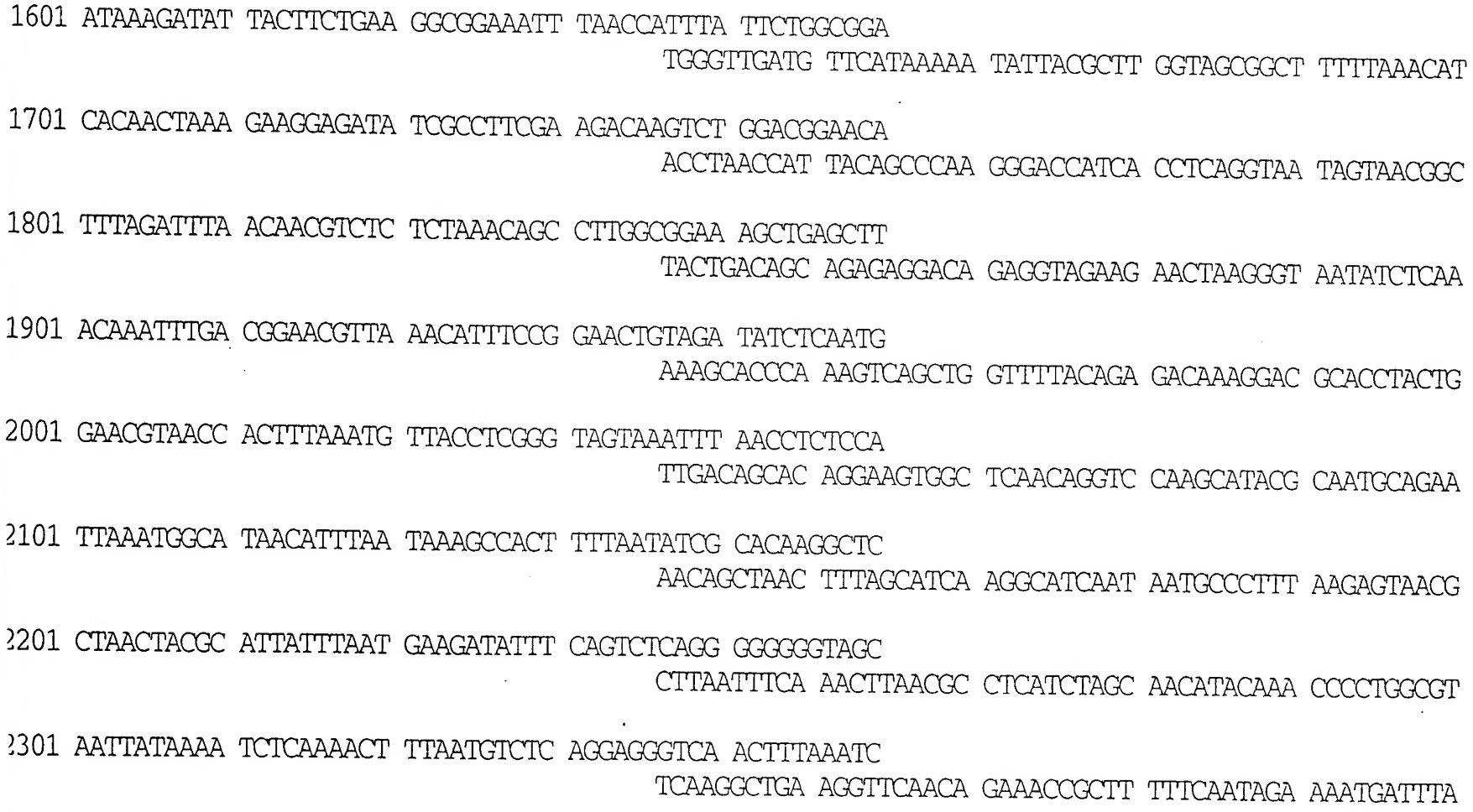

1601 ATAAAGATAT TACTTCTGAA GGCGGAAATT TAACCATTTA TTCTGGCGGA
TGGGTTGATG TTCATAAAAA TATTACGCTT GGTAGCGGCT TTTTAAACAT
1701 CACAACTAAA GAAGGAGATA TCGCCTTCGA AGACAAGTCT GGACGGAACA
ACCTAACCAT TACAGCCCAA GGGACCATCA CCTCAGGTAA TAGTAACGGC
1801 TTTAGATTTA ACAACGTCTC TCTAAACAGC CTTGGCGGAA AGCTGAGCTT
TACTGACAGC AGAGAGGACA GAGGTAGAAG AACTAAGGGT AATATCTCAA
1901 ACAAATTTGA CGGAACGTTA AACATTTCCG GAACTGTAGA TATCTCAATG
AAAGCACCCA AAGTCAGCTG GTTTTACAGA GACAAAGGAC GCACCTACTG
2001 GAACGTAACC ACTTTAAATG TTACCTCGGG TAGTAAATTT AACCTCTCCA
TTGACAGCAC AGGAAGTGGC TCAACAGGTC CAAGCATACG CAATGCAGAA
2101 TTAAATGGCA TAACATTTAA TAAAGCCACT TTTAATATCG CACAAGGCTC
AACAGCTAAC TTTAGCATCA AGGCATCAAT AATGCCCTTT AAGAGTAACG
2201 CTAACTACGC ATTATTTAAT GAAGATATTT CAGTCTCAGG GGGGGGTAGC
CTTAATTTCA AACTTAACGC CTCATCTAGC AACATACAAA CCCCTGGCGT
2301 AATTATAAAA TCTCAAAACT TTAATGTCTC AGGAGGGTCA ACTTTAAATC
TCAAGGCTGA AGGTTCAACA GAAACCGCTT TTTCAATAGA AAATGATTTA

FIG.8D

2401 AACTTAAACG CCACCGGTGG CAATATAACA ATCAGACAAG TCGAGGGTAC
CGATTCACGC GTCAACAAAG GTGTCGCAGC CAAAAAAAAC ATAACTTTTA

2501 AAGGGGGTAA TATCACCTTC GGCTCTCAAA AAGCCACAAC AGAAATCAAA
GGCAATGTTA CCATCAATAA AAACACTAAC GCTACTCTTT GTGGTGCGAA

2601 TTTTGCCGAA AACAAATCGC CTTTAAATAT AGCAGGAAAT GTTATTAATA
ATGGCAACCT TACCACTGCC GGCTCCATTA TCAATATAGC CGGAAATCTT

2701 ACTGTTTCAA AAGGCGCTAA CCTTCAAGCT ATAACAAATT ACACTTTTAA
TGTAGCCGGC TCATTTGACA ACAATGGCGC TTCAAACATT TCCATTGCCA

2801 GAGGAGGGGC TAAATTTAAA GATATCAATA ACACCAGTAG CTTAAATATT
ACCACCAACT CTGATACCAC TTACCGCACC ATTATAAAAG GCAATATATC

2901 CAACAAATCA GGTGATTTGA ATATTATTGA TAAAAAAAGC GACGCTGAAA
TCCAAATTGG CGGCAATATC TCACAAAAAG AAGGCAATCT CACAATTTCT

3001 TCTGATAAAG TAAATATTAC CAATCAGATA ACAATCAAAG CAGGCGTTGA
AGGGGGGCGT TCTGATTCAA GTGAGGCAGA AAATGCTAAC CTAACTATTC

3101 AAACCAAAGA GTTAAAATTG GCAGGAGACC TAAATATTTC AGGCTTTAAT
AAAGCAGAAA TTACAGCTAA AAATGGCAGT GATTTAACTA TTGGCAATGC

FIG.8E

3201 TAGCGGTGGT AATGCTGATG CTAAAAAAGT GACTTTTGAC AAGGTTAAAG
ATTCAAAAAT CTCGACTGAC GGTCACAATG TAACACTAAA TAGCGAAGTG

3301 AAAACGTCTA ATGGTAGTAG CAATGCTGGT AATGATAACA GCACCGGTTT
AACCATTTCC GCAAAAGATG TAACGGTAAA CAATAACGTT ACCTCCCACA

3401 AGACAATAAA TATCTCTGCC GCAGCAGGAA ATGTAACAAC CAAAGAAGGC
ACAACTATCA ATGCAACCAC AGGCAGCGTG GAAGTAACTG CTCAAAATGG

3501 TACAATTAAA GGCAACATTA CCTCGCAAAA TGTAACAGTG ACAGCAACAG
AAAATCTTGT TACCACAGAG AATGCTGTCA TTAATGCAAC CAGCGGCACA

3601 GTAAACATTA GTACAAAAAC AGGGGATATT AAAGGTGGAA TTGAATCAAC
TTCCGGTAAT GTAAATATTA CAGCGAGCGG CAATACACTT AAGGTAAGTA

3701 ATATCACTGG TCAAGATGTA ACAGTAACAG CGGATGCAGG AGCCTTGACA
ACTACAGCAG GCTCAACCAT TAGTGCGACA ACAGGCAATG CAAATATTAC

3801 AACCAAAACA GGTGATATCA ACGGTAAAGT TGAATCCAGC TCCGGCTCTG
TAACACTTGT TGCAACTGGA GCAACTCTTG CTGTAGGTAA TATTTCAGGT

3901 AACACTGTTA CTATTACTGC GGATAGCGGT AAATTAACCT CCACAGTAGG
TTCTACAATT AATGGGACTA ATAGTGTAAC CACCTCAAGC CAATCAGGCG

FIG.8F

4001 ATATTGAAGG TACAATTTCT GGTAATACAG TAAATGTTAC AGCAAGCACT GGTGATTTAA CTATTGGAAA TAGTGCAAAA GTTGAAGCGA AAAATGGAGC

4101 TGCAACCTTA ACTGCTGAAT CAGGCAAATT AACCACCCAA ACAGGCTCTA GCATTACCTC AAGCAATGGT CAGACAACTC TTACAGCCAA GGATAGCAGT

4201 ATCGCAGGAA ACATTAATGC TGCTAATGTG ACGTTAAATA CCACAGGCAC TTTAACTACT ACAGGGGATT CAAAGATTAA CGCAACCAGT GGTACCTTAA

4301 CAATCAATGC AAAAGATGCC AAATTAGATG GTGCTGCATC AGGTGACCGC ACAGTAGTAA ATGCAACTAA CGCAAGTGGC TCTGGTAACG TGACTGCGAA

4401 AACCTCAAGC AGCGTGAATA TCACCGGGGA TTTAAACACA ATAAATGGGT TAAATATCAT TTCGGAAAAT GGTAGAAACA CTGTGCGCTT AAGAGGCAAG

4501 GAAATTGATG TGAAATATAT CCAACCAGGT GTAGCAAGCG TAGAAGAGGT AATTGAAGCG AAACGCGTCC TTGAGAAGGT AAAAGATTTA TCTGATGAAG

4601 AAAGAGAAAC ACTAGCCAAA CTTGGTGTAA GTGCTGTACG TTTCGTTGAG CCAAATAATG CCATTACGGT TAATACACAA AACGAGTTTA CAACCAAACC

4701 ATCAAGTCAA GTGACAATTT CTGAAGGTAA GGCGTGTTTC TCAAGTGGTA ATGGCGCACG AGTATGTACC AATGTTGCTG ACGATGGACA GCAG

10092880 .030802

FIG.9A

```
  1 ATGAACAAGA TATATCGTCT CAAATTCAGC AAACGCCTGA ATGCTTTGGT
                                                TGCTGTGTCT GAATTGACAC GGGGTTGTGA CCATTCCACA GAAAAAGGCA

101 GTGAAAAACC TGTTCGTACG AAAGTACGCC ACTTGGCGTT AAAGCCACTT
                                                TCCGCTATAT TGCTATCTTT GGGCATGGCA TCCATTCCGC AATCTGTTTT

201 AGCGAGCGGT TTACAGGGAA TGAGCGTCGT ACACGGTACA GCAACCATGC
                                                AAGTAGACGG CAATAAAACC ACTATCCGTA ATAGCGTCAA TGCTATCATC

301 AATTGGAAAC AATTTAACAT TGACCAAAAT GAAATGGTGC AGTTTTTACA
                                                AGAAAGCAGC AACTCTGCCG TTTTCAACCG TGTTACATCT GACCAAATCT

401 CCCAATTAAA AGGGATTTTA GATTCTAACG GACAAGTCTT TTTAATCAAC
                                                CCAAATGGTA TCACAATAGG TAAAGACGCA ATTATTAACA CTAATGGCTT

501 TACTGCTTCT ACGCTAGACA TTTCTAACGA AAACATCAAG GCGCGTAATT
                                                TCACCCTTGA GCAAACCAAG GATAAAGCAC TCGCTGAAAT CGTGAATCAC

601 GGTTTAATTA CCGTTGGTAA AGACGGTAGC GTAAACCTTA TTGGTGGCAA
                                                AGTGAAAAAC GAGGGCGTGA TTAGCGTAAA TGGCGGTAGT ATTTCTTTAC

701 TTGCAGGGCA AAAAATCACC ATCAGCGATA TAATAAATCC AACCATCACT
                                                TACAGCATTG CTGCACCTGA AAACGAAGCG ATCAATCTGG GCGATATTTT
```


EP 0 955 368 A1

FIG.9B

801 TGCCAAAGGT GGTAACATTA ATGTCCGCGC TGCCACTATT CGCAATAAAG
GTAAACTTTC TGCCGACTCT GTAAGCAAAG ATAAAAGTGG TAACATTGTT

901 CTCTCTGCCA AAGAAGGTGA AGCGGAAATT GGCGGTGTAA TTTCCGCTCA
AAATCAGCAA GCCAAAGGTG GTAAGTTGAT GATTACAGGT GATAAAGTCA

1001 CATTAAAAAC AGGTGCAGTT ATCGACCTTT CAGGTAAAGA AGGGGGAGAG
ACTTATCTTG GCGGTGATGA GCGTGGCGAA GGTAAAAATG GTATTCAATT

1101 AGCGAAGAAA ACCTCTTTAG AAAAAGGCTC GACAATTAAT GTATCAGGCA
AAGAAAAAGG CGGGCGCGCT ATTGTATGGG GCGATATTGC ATTAATTAAT

1201 GGTAACATTA ATGCTCAAGG TAGCGATATT GCTAAAACTG GCGGCTTTGT
GGAAACATCA GGACATGACT TATCCATTGG TGATGATGTG ATTGTTGACG

1301 CTAAAGAGTG GTTATTAGAC CCAGATGATG TGTCCATTGA AACTCTTACA
TCTGGACGCA ATAATACCGG CGAAAACCAA GGATATACAA CAGGAGATGG

1401 GACTAAAGAG TCACCTAAAG GTAATAGTAT TTCTAAACCT ACATTAACAA
ACTCAACTCT TGAGCAAATC CTAAGAAGAG GTTCTTATGT TAATATCACT

1501 GCTAATAATA GAATTTATGT TAATAGCTCC ATCAACTTAT CTAATGGCAG
TTTAACACTT CACACTAAAC GAGATGGAGT TAAAATTAAC GGTGATATTA

FIG.9C

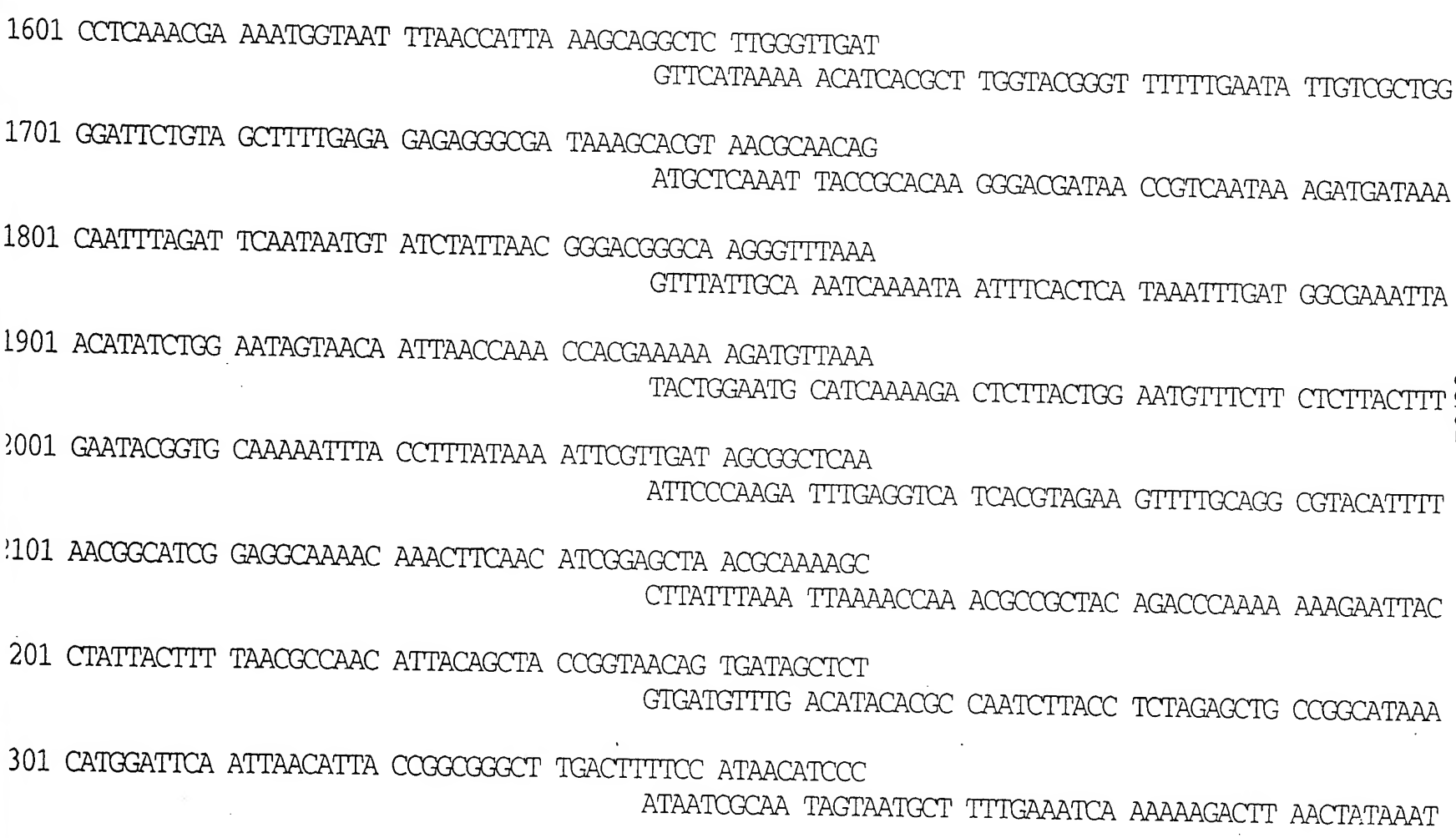

1601 CCTCAAACGA AAATGGTAAT TTAACCATTA AAGCAGGCTC TTGGGTTGAT
GTTCATAAAA ACATCACGCT TGGTACGGGT TTTTTGAATA TTGTCGCTGG
1701 GGATTCTGTA GCTTTTGAGA GAGAGGGCGA TAAAGCACGT AACGCAACAG
ATGCTCAAAT TACCGCACAA GGGACGATAA CCGTCAATAA AGATGATAAA
1801 CAATTTAGAT TCAATAATGT ATCTATTAAC GGGACGGGCA AGGGTTTAAA
GTTTATTGCA AATCAAAATA ATTTCACTCA TAAATTTGAT GGCGAAATTA
1901 ACATATCTGG AATAGTAACA ATTAACCAAA CCACGAAAAA AGATGTTAAA
TACTGGAATG CATCAAAAGA CTCTTACTGG AATGTTTCTT CTCTTACTTT
2001 GAATACGGTG CAAAAATTTA CCTTTATAAA ATTCGTTGAT AGCGGCTCAA
ATTCCCAAGA TTTGAGGTCA TCACGTAGAA GTTTTGCAGG CGTACATTTT
2101 AACGGCATCG GAGGCAAAAC AAACTTCAAC ATCGGAGCTA ACGCAAAAGC
CTTATTTAAA TTAAAACCAA ACGCCGCTAC AGACCCAAAA AAAGAATTAC
201 CTATTACTTT TAACGCCAAC ATTACAGCTA CCGGTAACAG TGATAGCTCT
GTGATGTTTG ACATACACGC CAATCTTACC TCTAGAGCTG CCGGCATAAA
301 CATGGATTCA ATTAACATTA CCGGCGGGCT TGACTTTTCC ATAACATCCC
ATAATCGCAA TAGTAATGCT TTTGAAATCA AAAAAGACTT AACTATAAAT

FIG.9D

2401 GCAACTGGCT CGAATTTTAG TCTTAAGCAA ACGAAAGATT CTTTTTATAA
TGAATACAGC AAACACGCCA TTAACTCAAG TCATAATCTA ACCATTCTTG

2501 GCGGCAATGT CACTCTAGGT GGGGAAAATT CAAGCAGTAG CATTACGGGC
AATATCAATA TCACCAATAA AGCAAATGTT ACATTACAAG CTGACACCAG

2601 CAACAGCAAC ACAGGCTTGA AGAAAAGAAC TCTAACTCTT GGCAATATAT
CTGTTGAGGG GAATTTAAGC CTAACTGGTG CAAATGCAAA CATTGTCGGC

2701 AATCTTTCTA TTGCAGAAGA TTCCACATTT AAAGGAGAAG CCAGTGACAA
CCTAAACATC ACCGGCACCT TTACCAACAA CGGTACCGCC AACATTAATA

2801 TAAAACAAGG AGTGGTAAAA CTCCAAGGCG ATATTATCAA TAAAGGTGGT
TTAAATATCA CTACTAACGC CTCAGGCACT CAAAAAACCA TTATTAACGG

2901 AAATATAACT AACGAAAAAG GCGACTTAAA CATCAAGAAT ATTAAAGCCG
ACGCCGAAAT CCAAATTGGC GGCAATATCT CACAAAAAGA AGGCAATCTC

3001 ACAATTTCTT CTGATAAAGT AAATATTACC AATCAGATAA CAATCAAAGC
AGGCGTTGAA GGGGGGCGTT CTGATTCAAG TGAGGCAGAA AATGCTAACC

3101 TAACTATTCA AACCAAAGAG TTAAAATTGG CAGGAGACCT AAATATTTCA
GGCTTTAATA AAGCAGAAAT TACAGCTAAA AATGGCAGTG ATTTAACTAT

3201 TGGCAATGCT AGCGGTGGTA ATGCTGATGC TAAAAAAGTG ACTTTTGACA
AGGTTAAAGA TTCAAAAATC TCGACTGACG GTCACAATGT AACACTAAAT

FIG.9E

```
3301 AGCGAAGTGA AAACGTCTAA TGGTAGTAGC AATGCTGGTA ATGATAACAG
                                        CACCGGTTTA ACCATTTCCG CAAAAGATGT AACGGTAAAC AATAACGTTA

3401 CCTCCCACAA GACAATAAAT ATCTCTGCCG CAGCAGGAAA TGTAACAACC
                                        AAAGAAGGCA CAACTATCAA TGCAACCACA GGCAGCGTGG AAGTAACTGC

3501 TCAAAATGGT ACAATTAAAG GCAACATTAC CTCGCAAAAT GTAACAGTGA
                                        CAGCAACAGA AAATCTTGTT ACCACAGAGA ATGCTGTCAT TAATGCAACC

3601 AGCGGCACAG TAAACATTAG TACAAAAACA GGGGATATTA AAGGTGGAAT
                                        TGAATCAACT TCCGGTAATG TAAATATTAC AGCGAGCGGC AATACACTTA

3701 AGGTAAGTAA TATCACTGGT CAAGATGTAA CAGTAACAGC GGATGCAGGA
                                        GCCTTGACAA CTACAGCAGG CTCAACCATT AGTGCGACAA CAGGCAATGC

3801 AAATATTACA ACCAAAACAG GTGATATCAA CGGTAAAGTT GAATCCAGCT
                                        CCGGCTCTGT AACACTTGTT GCAACTGGAG CAACTCTTGC TGTAGGTAAT

3901 ATTTCAGGTA ACACTGTTAC TATTACTGCG GATAGCGGTA AATTAACCTC
                                        CACAGTAGGT TCTACAATTA ATGGGACTAA TAGTGTAACC ACCTCAAGCC

4001 AATCAGGCGA TATTGAAGGT ACAATTTCTG GTAATACAGT AAATGTTACA
                                        GCAAGCACTG GTGATTTAAC TATTGGAAAT AGTGCAAAAG TTGAAGCGAA
```

FIG.9F

```
4101 AAATGGAGCT GCAACCTTAA CTGCTGAATC AGGCAAATTA ACCACCCAAA
                                                CAGGCTCTAG CATTACCTCA AGCAATGGTC AGACAACTCT TACAGCCAAG

4201 GATAGCAGTA TCGCAGGAAA CATTAATGCT GCTAATGTGA CGTTAAATAC
                                                CACAGGCACT TTAACTACTA CAGGGGATTC AAAGATTAAC GCAACCAGTG

4301 GTACCTTAAC AATCAATGCA AAAGATGCCA AATTAGATGG TGCTGCATCA
                                                GGTGACCGCA CAGTAGTAAA TGCAACTAAC GCAAGTGGCT CTGGTAACGT

4401 GACTGCGAAA ACCTCAAGCA GCGTGAATAT CACCGGGGAT TTAAACACAA
                                                TAAATGGGTT AAATATCATT TCGGAAAATG GTAGAAACAC TGTGCGCTTA

4501 AGAGGCAAGG AAATTGATGT GAAATATATC CAACCAGGTG TAGCAAGCGT
                                                AGAAGAGGTA ATTGAAGCGA AACGCGTCCT TGAGAAGGTA AAAGATTTAT

4601 CTGATGAAGA AAGAGAAACA CTAGCCAAAC TTGGTGTAAG TGCTGTACGT
                                                TTCGTTGAGC CAAATAATGC CATTACGGTT AATACACAAA ACGAGTTTAC

4701 AACCAAACCA TCAAGTCAAG TGACAATTTC TGAAGGTAAG GCGTGTTTCT
                                                CAAGTGGTAA TGGCGCACGA GTATGTACCA ATGTTGCTGA CGATGGACAG

4801 CAG
```


EP 0 954 581 B1

FIG.10A

COMPARISON OF DERIVED AMINO ACID SEQUENCE

	1				50
Hmw3com	MNKIYRLKFS	KRLNALVAVS	ELTRGCDHST	EKGSEKPVRT	KVRHLALKPL
Hmw4com	MNKIYRLKFS	KRLNALVAVS	ELTRGCDHST	EKGSEKPVRT	KVRHLALKPL
Hmw1com	MNKIYRLKFS	KRLNALVAVS	ELTRGCDHST	EKGSEKPVRT	KVRHLALKPL
Hmw2com	MNKIYRLKFS	KRLNALVAVS	ELTRGCDHST	EKGSEKPVRT	KVRHLALKPL

	51				100
Hmw3com	SAILLSLGMA	SIPQSVLASG	LQGMSVVHGT	ATMQVDGNKT	TIRNSVNAII
Hmw4com	SAILLSLGMA	SIPQSVLASG	LQGMSVVHGT	ATMQVDGNKT	TIRNSVNAII
Hmw2com	SAMLLSLGVT	SIPQSVLASG	LQGMSVVHGT	ATMQVDGNKT	TIRNSVNAII
Hmw2com	SAMLLSLGVT	SIPQSVLASG	LQGMSVVHGT	ATMQVDGNKT	TIRNSVNAII

FIG.10B

	101				150
Hmw3com	NWKQFNIDQN	EMEQFLQESS	NSAVFNRVTS	DQISQLKSIL	DSNSQVFLIN
Hmw4com	NWKQFNIDQN	EMEQFLQESS	NSAVFNRVTS	DQISQLKGIL	DSNSQVFLIN
Hmw1com	NWKQFNIDQN	EMVQFLQENN	NSAVFNRVTS	NQISQLKGIL	DSNSQVFLIN
Hmw2com	NWKQFNIDQN	EMVQFLQENN	NSAVFNRVTS	NQISQLKGIL	DSNSQVFLIN

	151				200
Hmw3com	PNGITIGKDA	IINTNSFTAS	TLDISNENIK	ARNFTLEQTK	DKALAEIVNH
Hmw4com	PNGITIGKDA	IINTNSFTAS	TLDISNENIK	ARNFTLEQTK	DKALAEIVNH
Hmw1com	PNGITIGKDA	IINTNSFTAS	TLDISNENIK	ARNFTLEQTK	DKALAEIVNH
Hmw2com	PNGITIGKDA	IINTNSFTAS	TLDISNENIK	ARNFTLEQTK	DKALAEIVNH

FIG.10C

	201				250
Hmw3com	GLITVGKDGS	VNLIGGKVKN	EGVISVNGGS	ISLLAGQKIT	ISDIINPTIT
Hmw4com	GLITVGKDGS	VNLIGGKVKN	EGVISVNGGS	ISLLAGQKIT	ISDIINPTIT
Hmw1com	GLITVGKDGS	VNLIGGKVKN	EGVISVNGGS	ISLLAGQKIT	ISDIINPTIT
Hmw2com	GLITVGKDGS	VNLIGGKVKN	EGVISVNGGS	ISLLAGQKIT	ISDIINPTIT

	251				300
Hmw3com	YSIAAPENEA	INLGDIFAKG	GNIINVRAATI	RNKGKLSADS	VSKDKSGNIV

FIG. 10D.

```
Hmw4com   YSIAAPENEA INLGDIFAKG GNINVRAATI RNKGKLSADS VSKDKSGNIV
Hmw1com   YSIAAPENEA VNLGDIFAKG GNINVRAATI RNKGKLSADS VSKDKSGNIV
Hmw2com   YSIAAPENEA VNLGDIFAKG GNINVRAATI RNKGKLSADS VSKDKSGNIV

          301                                                350
Hmw3com   LSAKEGEAEI GGVISAQNQQ AKGGKLMITG DKVTLKTGAV IDLSGKEGGE
Hmw4com   LSAKEGEAEI GGVISAQNQQ AKGGKLMITG DKVTLKTGAV IDLSGKEGGE
Hmw1com   LSAKEGEAEI GGVISAQNQQ AKGGKLMITG DKVTLKTGAV IDLSGKEGGE
Hmw2com   LSAKEGEAEI GGVISAQNQQ AKGGKLMITG DKVTLKTGAV IDLSGKEGGE

          351                                                400
Hmw3com   TYLGGDERGE GKNGIQLAKK TTLEKGSTIN VSGKEKGGRA IVWGDIALID
Hmw4com   TYLGGDERGE GKNGIQLAKK TTLEKGSTIN VSGKEKGGRA IVWGDIALID
Hmw1com   TYLGGDERGE GKNGIQLAKK TTLEKGSTIN VSGKEKGGRA IVWGDIALID
Hmw2com   TYLGGDERGE GKNGIQLAKK TTLEKGSTIN VSGKEKGGRA IVWGDIALID
```

FIG.10E.

```
                401                                                 450
Hmw3com   GNINAQGK.D IAKTGGFVET SGHYLSIDDN AIVKTKEWLL DPENVTIEAP
Hmw4com   GNINAQGS.D IAKTGGFVET SGHDLSIGDD VIVDAKEWLL DPDDVSIETL
Hmw1com   GNINAQGSGD IAKTGGFVET SGHDLFIKDN AIVDAKEWLL DPDNVTINAE
Hmw2com   GNINAQGSGD IAKTGGFVET SGHYLSIESN AIVKTKEWLL DPDDVTIEAE

                451                                                 500
Hmw3com   SASRVELGAD RNSHSAEVIK VTLKKNNTSL TTLTNTTISN LLKSAHVVNI
Hmw4com   TSGRNNTGEN QGYTTGDGTK ESPKGNSISK PTLTNSTLEQ ILRRGSYVNI
Hmw1com   TAGRSNTSED DEYTGSGNSA STPKRNKE.K TTLTNTTLES ILKKGTFVNI
Hmw2com   DPLRNNTGIN DEFPTGTGEA SDPKKNSELK TTLTNTTISN YLKNAWTMNI

                501                                                 550
Hmw3com   TARRKLTVNS SISIERGSHL ILHSEGQGGQ GVQIDKDITS .E...GGNLT
Hmw4com   TANNRIYVNS SINLSNGS.L TLHTK...RD GVKINGDITS NE...NGNLT
Hmw1com   TANQRIYVNS SINL.SNGSL TLWSEGRSGG GVEINNDITT GDDTRGANLT
Hmw2com   TASRKLTVNS SINGSNGSHL ILHSKGQRGG GVQIDGDIT. ...SKGGNLT
```

FIG.10F.

```
                551                                                    600
Hmw3com   IYSGGWVDVH KNITLGS.GF LNITTKEGDI AFEDKSGR..  ..NNLTITAQ
Hmw4com   IKAGSWVDVH KNITLGT.GF LNIVAGDS.V AFEREGDKAR NATDAQITAQ
Hmw1com   IYSGGWVDVH KNISLGAQGN INITAKQD.I AFEKGSNQV.  ......ITGQ
Hmw2com   IYSGGWVDVH KNITLD.QGF LNITA.AS.V AFEGGNNKAR DANNLTITAQ

                601                                                    650
Hmw3com   GTITSG.NSN GFRFNNVSLN SLGGKLSFTD SREDRGRRTK GNISNKFDGT
Hmw4com   GTITVNKDDK QFRFNNVSIN GTGKGLKFIA NQN.......  .NFTHKFDGE
Hmw1com   GTIT.SGNQK GFRFNNVSLN GTGSGLQFTT KRTN.....K YAITNKFEGT
Hmw2com   GTVTITGEGK DFRANNVSLN GTGKGLNIIS SVNN......  ..LTHNLSGT

                651                                                    700
Hmw3com   LNISGTVDIS MKAPKVSWFY RD.KGRTYWN VTTLNVTSGS KFNLSIDSTG
Hmw4com   INISGIVTIN QTTKKDVKYW NA.SKDSYWN VSSLTLNTVQ KFTF.IKFVD
Hmw1com   LNISGKVNIS MVLPKNESGY DKFKGRTYWN LTSLNVSESG EFNLTIDSRG
```

FIG.10G.

```
Hmw2com   INISGNITIN QTTRKNTSYW QTSHD.SHWN VSALNLETGA NFTF.IKYIS

          701                                                 750
Hmw3com   SGSTG...PS IRNA..ELNG ITFN....KA TFNIAQGSTA NFSIKASIMP
Hmw4com   SGSNS...QD LRSSRRSFAG VHFNGIGGKT NFNIGANAKA LFKLKPNAAT
Hmw1com   SDSAGTLTQ. ....PYNLNG ISFN...KDT TFNVERNARV NFDIKAPIGI
Hmw2com   SNSKGLTTQY RSSAGVNFNG V..N...GNM SFNLKEGAKV NFKLKPNENM

          751                                                 800
Hmw3com   FKSNANYAL. FNEDISVSG. .GGSVNFKLN ASSSNIQTPG VIIKSQNFNV
Hmw4com   DPKKELPIT. FNANITATGN SDSSVMFDIH A...NLTSRA AGINMDSINI
Hmw1com   NKYSSLNYAS FNGNISVSG. .GGSVDFTLL ASSSNVQTPG VVINSKYFNV
Hmw2com   NTSKPLPI.R FLANITATG. .GGSVFFDIY ANHS...GRG AELKMSEINI

          801                                                 850
Hmw3com   SGGSTLNLKA EGSTETAFSI ENDLNLNATG GNITIRQVEG T..DSRVNKG
Hmw4com   TGGLDFSITS HNRNSNAFEI KKDLTINATG SNFSLKQTKD SFYNEYSKHA
```

FIG.10H.

```
Hmw1com   STGSSLRFKT SGSTKTGFSI EKDLTLNATG GNITLLQVEG T..DGMIGKG
Hmw2com   SNGANFTLNS HVRGDDAFKI NKDLTINATN SNFSLRQTKD DFYDGYARNA

                851                                          900
Hmw3com   VAAKKNITFK GGNITFGSQK ATTEIKGNVT INKNTNATLR GANFAEN...
Hmw4com   INSSHNLTIL GGNVTLGGEN SSSSITGNIN ITNKANVTLQ ADTSNSNTGL
Hmw1com   IVAKKNITFE GGNITFGSRK AVTEIEGNVT INNNANVTLI GSDFDNHQ..
Hmw2com   INSTYNISIL GGNVTLGGQN SSSSITGNIT IEKAANVTLE ANNAPNQQNI

                901                                          950
Hmw3com   KSPLNIAGNV INNGNLTTAG SIINIAGNLT VSKGANLQAI TNYTFNVAGS
Hmw4com   KKRTLTLGNI SVEGNLSLTG ANANIVGNLS IAEDSTFKGE ASDNLNITGT
Hmw1com   KPLTIKKDVI INSGNLTAGG NIVNIAGNLT VESNANFKAI TNFTFNVGGL
Hmw2com   RDRVIKLGSL LVNGSLSLTG ENADIKGNLT ISESATFKGK TRDTLNITGN

                951                                         1000
```

FIG.10I.

Hmw3com	FDNNGASNIS	IARGGAKFK.	DINNTSSLNI	TTNSDTTYRT	IIKGNISNKS
Hmw4com	FTNNGTANIN	IKQGVVKLQG	DINNKGGLNI	TTNASGTQKT	IINGNITNEK
Hmw1com	FDNKGNSNIS	IAKGGARFK.	DIDNSKNLSI	TTNSSSTYRT	IISGNITNKN
Hmw2com	FTNNGTAEIN	ITQGVVKLG.	NVTNDGDLNI	TTHAKRNQRS	IIGGDIINNK

1001 1050

Hmw3com	GDLNIIDKKS	DAEIQIGGNI	SQKEGNLTIS	SDKVNITNQI	TIKAGVEGGR
Hmw4com	GDLNIKNIKA	DAEIQIGGNI	SQKEGNLTIS	SDKVNITNQI	TIKAGVEGGR
Hmw1com	GDLNITNEGS	DTEMQIGGDI	SQKEGNLTIS	SDKINITKQI	TIKAGVDGEN
Hmw2com	GSLNITDSNN	DAEIQIGGNI	SQKEGNLTIS	SDKINITKQI	TIKKGIDGED

1051 1100

Hmw3com	SDSSEAENAN	LTIQTKELKL	AGDLNISGFN	KAEITAKNGS	DLTIGNASGG
Hmw4com	SDSSEAENAN	LTIQTKELKL	AGDLNISGFN	KAEITAKNGS	DLTIGNASGG
Hmw1com	SDSDATNNAN	LTIKTKELKL	TQDLNISGFN	KAEITAKDGS	DLTIGNTNSA
Hmw2com	SSSDATSNAN	LTIKTKELKL	TEDLSISGFN	KAEITAKDGR	DLTIGNSNDG

FIG.10J.

```
                1101                                                1150
Hmw3com   N..ADAKKVT FDKVKDSKIS TDGHNVTLNS EVKT..SNGS SNAGNDNSTG
Hmw4com   N..ADAKKVT FDKVKDSKIS TDGHNVTLNS EVKT..SNGS SNAGNDNSTG
Hmw1com   D.GTNAKKVT FNQVKDSKIS ADGHKVTLHS KVETSGSNNN TEDSSDNNAG
Hmw2com   NSGAEAKKVT FNNVKDSKIS ADGHNVTLNS KVKTSSSNGG RESNSDNDTG

                1151                                                1200
Hmw3com   LTISAKDVTV NNNVTSHKTI NISAAAGNVT TKEGTTINAT TGSVEVTAQN
Hmw4com   LTISAKDVTV NNNVTSHKTI NISAAAGNVT TKEGTTINAT TGSVEVTAQN
Hmw1com   LTIDAKNVTV NNNITSHKAV SISATSGEIT TKTGTTINAT TGNVEIT...
Hmw2com   LTITAKNVEV NKDVTSLKTV NITA.SEKVT TTAGSTINAT NGKASIT...

                1201                                                1250
Hmw3com   GTIKGNITSQ NVTVTATENL VTTENAVINA TSGTVNISTK TGDIKGGIES
Hmw4com   GTIKGNITSQ NVTVTATENL VTTENAVINA TSGTVNISTK TGDIKGGIES
Hmw1com   .......... .......... .......... ........AQ TGDIKGGIES
```

FIG.10K.

```
Hmw2com   ..... ..... ..... .....TK T.....

          1251                                                1300
Hmw3com   TSGNVNITAS GNTLKVSNIT GQDVTVTADA GALTTTAGST ISATTGNANI
Hmw4com   TSGNVNITAS GNTLKVSNIT GQDVTVTADA GALTTTAGST ISATTGNANI
Hmw1com   SSGSVTLTAT EGALAVSNIS GNTVTVTANS GALTTLAGST IKG.TESVTT
Hmw2com   ..... ..... ..... ..... .....

          1301                                                1350
Hmw3com   TTKTGDINGK VESSSGSVTL VATGATLAVG NISGNTVTIT ADSGKLTSTV
Hmw4com   TTKTGDINGK VESSSGSVTL VATGATLAVG NISGNTVTIT ADSGKLTSTV
Hmw1com   SSQSGDIG.. ..... .....G TISGGTVEVK ATESLTTQSN
Hmw2com   ....GDIS.. ..... .....G TISGNTVSVS ATVDLTTKSG

          1351                                                1400
Hmw3com   GSTINGTNSV TTSSQSGDIE GTISGNTVNV TASTGDLTIG NSAKVEAKNG
Hmw4com   GSTINGTNSV TTSSQSGDIE GTISGNTVNV TASTGDLTIG NSAKVEAKNG
```

FIG.10L.

```
Hmw1com   SKIKATTGEA NVTSATGTIG GTISGNTVNV TANAGDLTVG NGAEINATEG
Hmw2com   SKIEAKSGEA NVTSATGTIG GTISGNTVNV TANAGDLTVG NGAEINATEG

                1401                                          1450
Hmw3com   AATLTAESGK LTTQTGSSIT SSNGQTTLTA KDSSIAGNIN AANVTLNTTG
Hmw4com   AATLTAESGK LTTQTGSSIT SSNGQTTLTA KDSSIAGNIN AANVTLNTTG
Hmw1com   AATLTTSSGK LTTEASSHIT SAKGQVNLSA QDSSVAGSIN AANVTLNTTG
Hmw2com   AATLTATGNT LTTEAGSSIT STKGQVDLLA QNSSIAGNIN AANVTLNTTG

                1451                                          1500
Hmw3com   TLTTTGDSKI NATSGTLTIN AKDAKLDGAA SGDRTVVNAT NASGSGNVTA
Hmw4com   TLTTTGDSKI NATSGTLTIN AKDAKLDGAA SGDRTVVNAT NASGSGNVTA
Hmw1com   TLTTVKGSNI NATSGTLTIN AKDAELNGAA LGNHTVVNAT NANGSGSVIA
Hmw2com   TLTTVAGSDI KATSGTLTIN AKDAKLNGDA SGDSTEVNAV NASGSGSVTA

                1501                                          1550
```

FIG.10M.

```
Hmw3com   KTSSSVNITG DLNTINGLNI ISENGRNTVR LRGKEIDVKY IQPGVASVEE
Hmw4com   KTSSSVNITG DLNTINGLNI ISENGRNTVR LRGKEIDVKY IQPGVASVEE
Hmw1com   TTSSRVNITG DLITINGLNI ISKNGINTVL LKGVKIDVKY IQPGIASVDE
Hmw2com   ATSSSVNITG DLNTVNGLNI ISKDGRNTVR LRGKEIEVKY IQPGVASVEE

                1551                                          1600
Hmw3com   VIEAKRVLEK VKDLSDEERE TLAKLGVSAV RFVEPNNAIT VNTQNEFTTK
Hmw4com   VIEAKRVLEK VKDLSDEERE TLAKLGVSAV RFVEPNNAIT VNTQNEFTTK
Hmw1com   VIEAKRILEK VKDLSDEERE ALAKLGVSAV RFIEPNNTIT VDTQNEFATR
Hmw2com   VIEAKRVLEK VKDLSDEERE TLAKLGVSAV RFVEPNNTIT VNTQNEFTTR

                1601                          1632
Hmw3com   PSSQVTISEG KACFSSGNGA RVCTNVADDG QQ   ( SEQ ID No: 9 )
Hmw4com   PSSQVTISEG KACFSSGNGA RVCTNVADDG QQ   ( SEQ ID No: 10)
Hmw1com   PLSRIVISEG RACFSNSDGA TVCVNIADNG R.   ( SEQ ID No: 2)
Hmw2com   PSSQVIISEG KACFSSGNGA RVCTNVADDG QP   ( SEQ ID No: 4)
```

AMENDED SHEET

FIG.10M.

```
Hmw3com   KTSSSVNITG DLNTINGLNI ISENGRNTVR LRGKEIDVKY IQPGVASVEE
Hmw4com   KTSSSVNITG DLNTINGLNI ISENGRNTVR LRGKEIDVKY IQPGVASVEE
Hmw1com   TTSSRVNITG DLITINGLNI ISKNGINTVL LKGVKIDVKY IQPGIASVDE
Hmw2com   ATSSSVNITG DLNTVNGLNI ISKDGRNTVR LRGKEIEVKY IQPGVASVEE

                1551                                          1600
Hmw3com   VIEAKRVLEK VKDLSDEERE TLAKLGVSAV RFVEPNNAIT VNTQNEFTTK
Hmw4com   VIEAKRVLEK VKDLSDEERE TLAKLGVSAV RFVEPNNAIT VNTQNEFTTK
Hmw1com   VIEAKRILEK VKDLSDEERE ALAKLGVSAV RFIEPNNTIT VDTQNEFATR
Hmw2com   VIEAKRVLEK VKDLSDEERE TLAKLGVSAV RFVEPNNTIT VNTQNEFTTR

                1601                                  1632
Hmw3com   PSSQVTISEG KACFSSGNGA RVCTNVADDG QQ
Hmw4com   PSSQVTISEG KACFSSGNGA RVCTNVADDG QQ
Hmw1com   PLSRIVISEG RACFSNSDGA TVCVNIADNG R.
Hmw2com   PSSQVIISEG KACFSSGNGA RVCTNVADDG QP
```

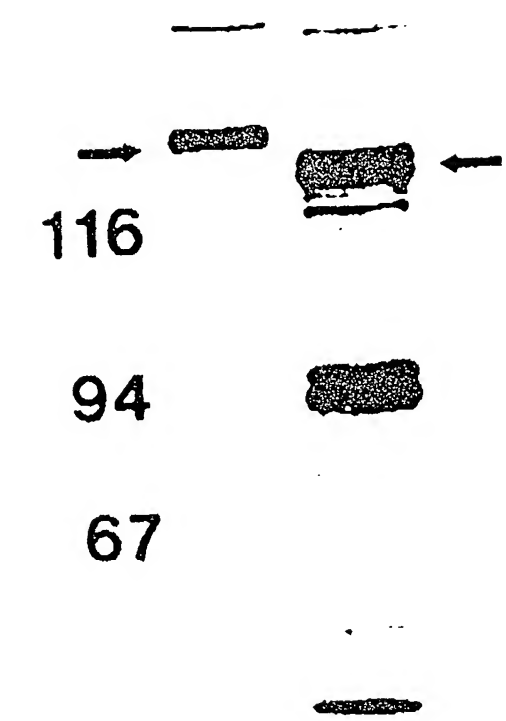


FIG. 11

WESTERN IMMUNOBLOT ASSAY OF PHAGE LYSATES CONTAINING EITHER THE HMW1 OR HMW2 RECOMBINANT PROTEINS. LYSATES WERE PROBED WITH AN *E. COLI*-ABSORBED ADULT SERUM SAMPLE WITH HIGH-TITER ANTIBODY AGAINST HIGH-MOLECULAR-WEIGHT PROTEINS. THE ARROWS INDICATE THE MAJOR IMMUNOREACTIVE PROTEIN BANDS OF 125 AND 120 kDa IN THE HMW1 AND HMW2 LYSATES, RESPECTIVELY.

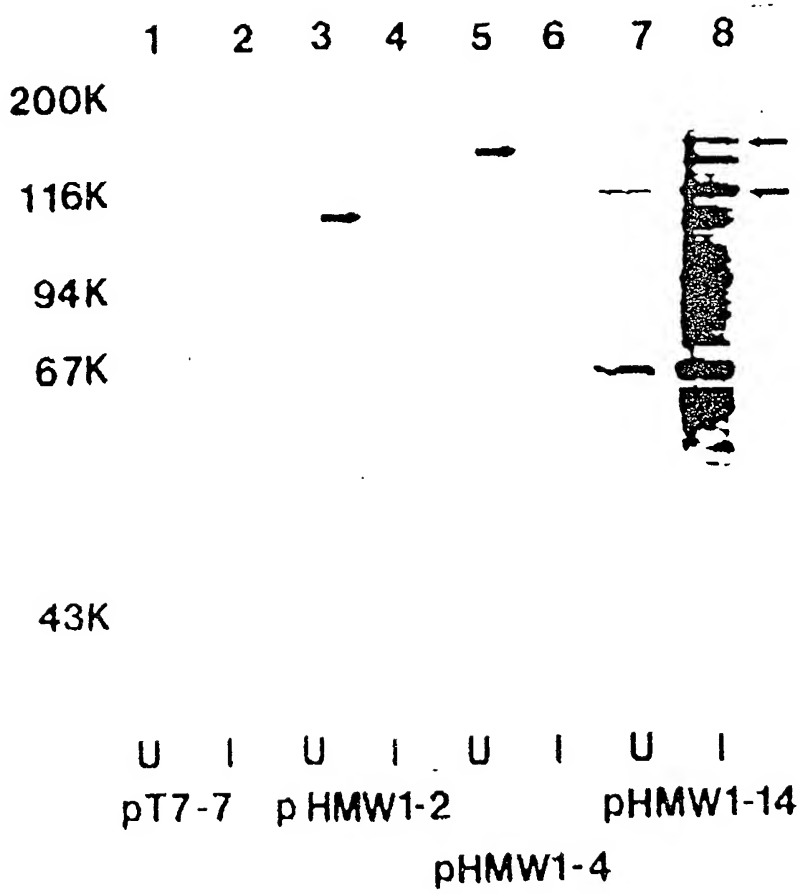


FIG. 12

WESTERN IMMUNOBLOT ASSAY OF CELL SONICATES PREPARED FROM *E. COLI* TRANSFORMED WITH PLASMID pT7-7 (LANES 1 AND 2) pHMW1-2 (LANES 3 AND 4), pHMW1-4 (LANES 5 AND 6), OR pHMW1-14 (LANES 7 AND 8). THE SONICATES WERE PROBED WITH AN *E. COLI*-ABSORBED ADULT SERUM SAMPLE WITH HIGH -TITER ANTIBODY AGAINST HIGH - MOLECULAR -WEIGHT PROTEINS. LANES LABELED U AND I REPRESENT SONICATES PREPARED BEFORE AND AFTER INDUCTION OF THE GROWING SAMPLES WITH IPTG, RESPECTIVELY. THE ARROWS INDICATE PROTEIN BANDS OF INTEREST AS DESCRIBED IN THE TEXT.

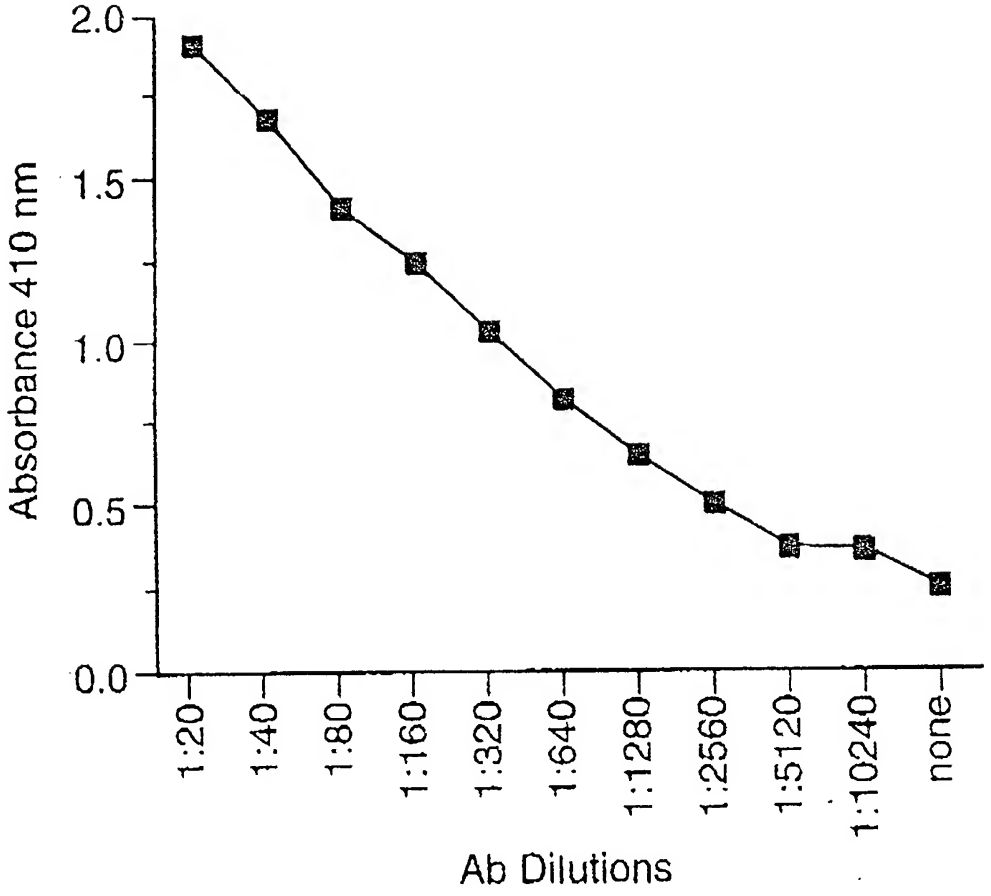


FIG. 13

ELISA WITH rHMW1 ANTISERUM ASSAYED AGAINST PURIFIED FILAMENTOUS HEMAGLUTININ OF B. *PERTUSSIS*. Ab, ANTIBODY.

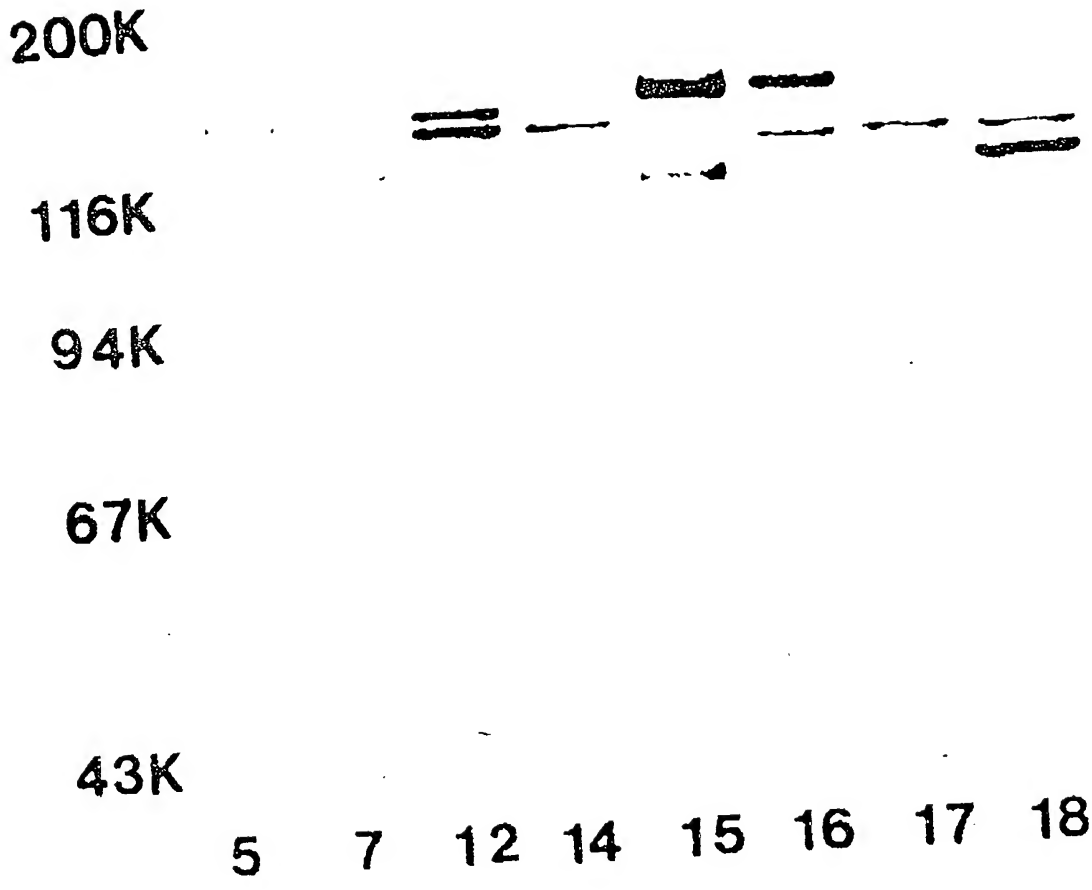


FIG. 14
WESTERN IMMUNOBLOT ASSAY OF CELL SONICATES FROM A PANEL OF EPIDEMIOLOGICALLY UNRELATED NONTYPEABLE *H. INFLUENZAE* STRAINS.THE SONICATES WERE PROBED WITH RABBIT ANTISERUM PREPARED AGAINST HMW1-4 RECOMBINANT PROTEIN. THE STRAIN DESIGNATIONS ARE INDICATED BY THE NUMBERS BELOW EACH LANE.

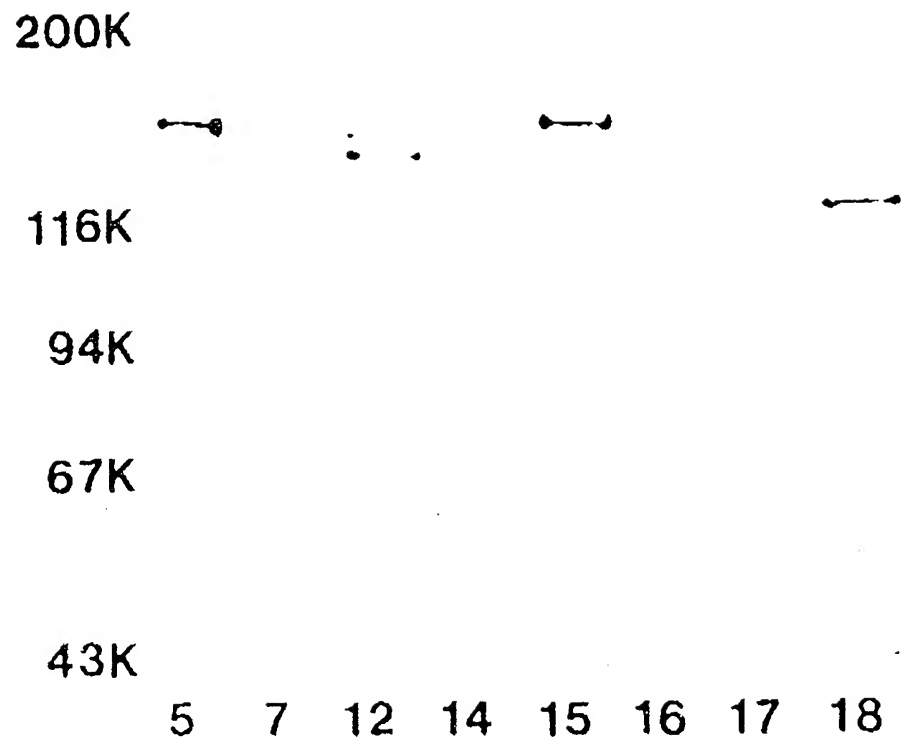


FIG. 15

WESTERN IMMUNOBLOT ASSAY OF CELL SONICATES FROM A PANEL OF EPIDEMIOLOGICALLY UNRELATED NONTYPEABLE H. *INFLUENZAE* STRAINS.THE SONICATES WERE PROBED WITH MONOCLONAL ANTIBODY X3C, A MURINE IgG ANTIBODY WHICH RECOGNIZES THE FILAMENTOUS HEMAGGLUTININ OF *B. PERTUSSIS* (13).THE STRAIN DESIGNATIONS ARE INDICATED BY THE NUMBERS BELOW EACH LANE.

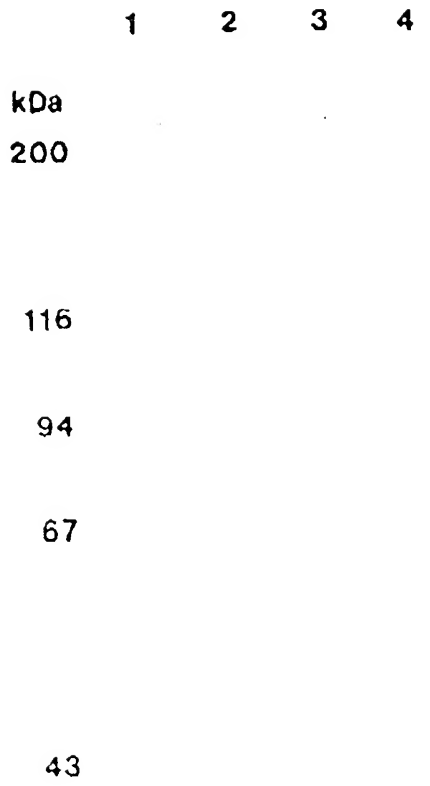
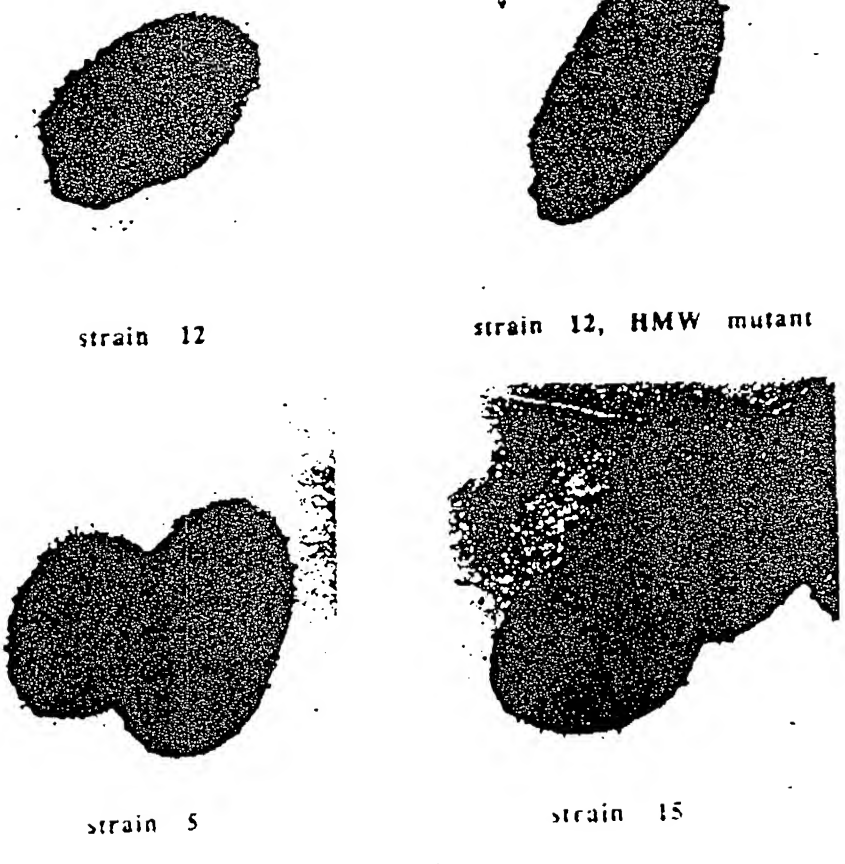


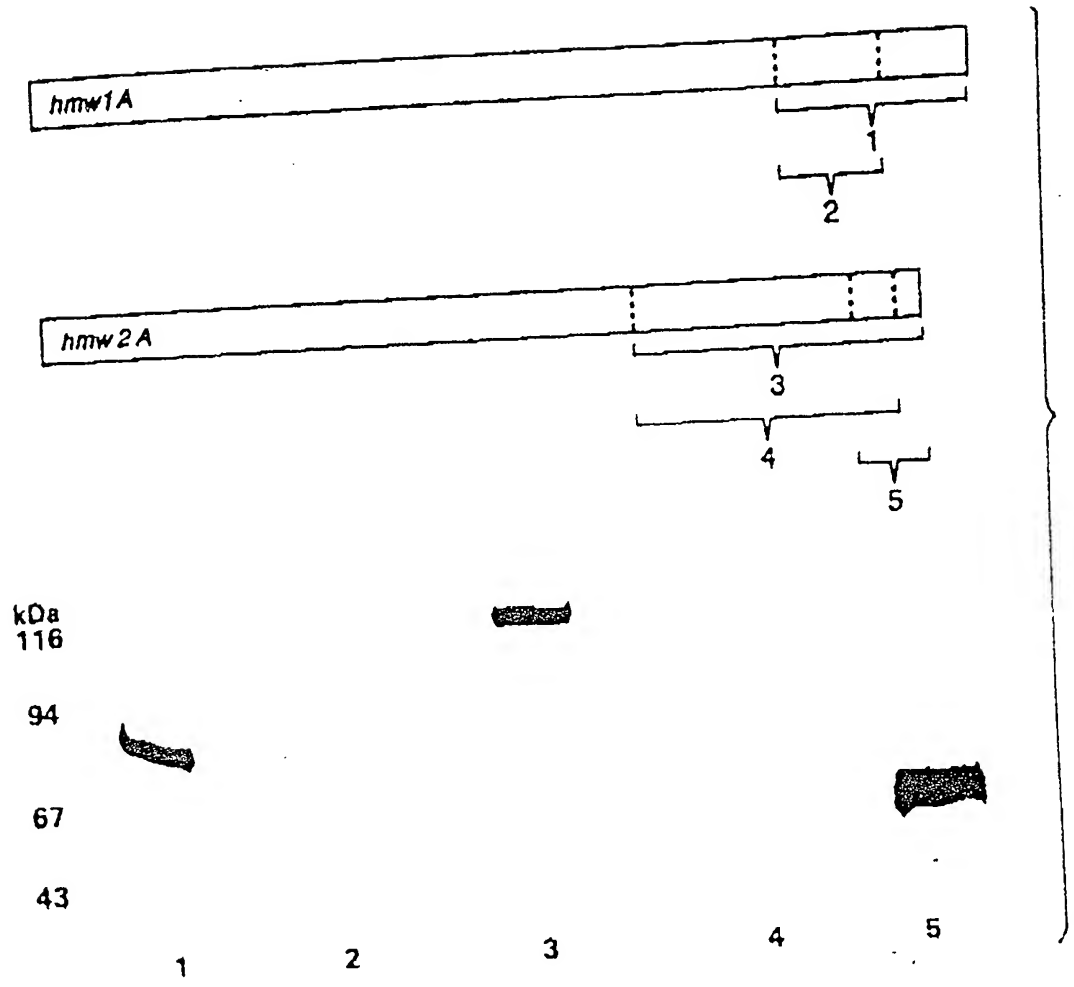
FIG. 16

IMMUNOBLOT ASSAY OF CELL SONICATES OF NONTYPABLE *H. INFLUENZAE* STRAIN 12 DERIVATIVES. THE SONICATES WERE PROBED WITH RABBIT ANTISERUM PREPARED AGAINST HMW-1 RECOMBINANT PROTEIN. LANES: 1, WILD-TYPE STRAIN; 2, HMW-2$^-$ MUTANT; 3, HMW-1$^-$ MUTANT; 4, HMW-1$^-$ / HMW-2$^-$ DOUBLE MUTANT.



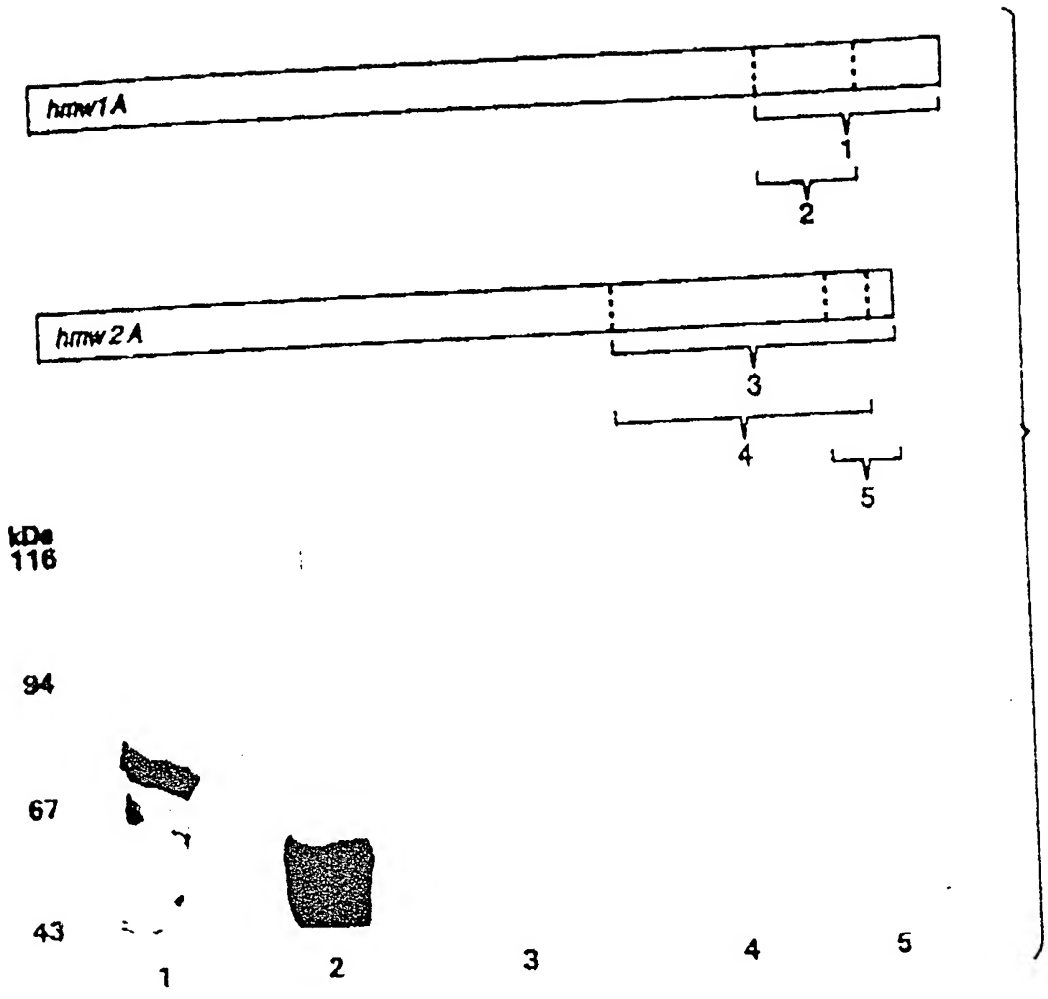
IMMUNOELECTRON MICROSCOPY WITH Mab AD6

FIG.20



WESTERN IMMUNOBLOT ASSAY WITH Mab AD6 AND HMW1A OR HMW2A RECOMBINANT PROTEINS

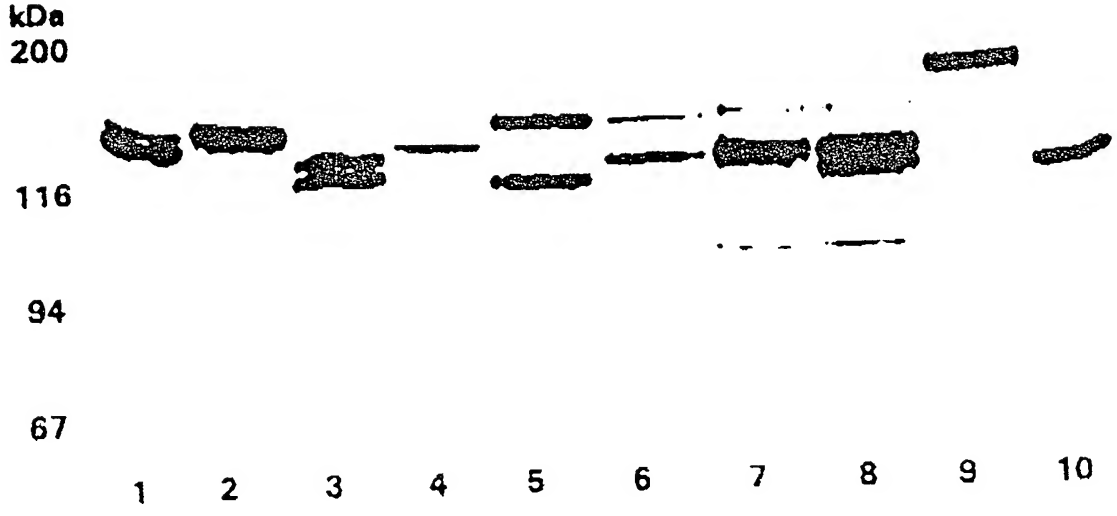
FIG.21



WESTERN IMMUNOBLOT ASSAY WITH Mab 10C5 AND HMW1A OR HMW2A RECOMBINANT PROTEINS

FIG.22

IPEA/US 21 APR 1998



WESTERN IMMUNOBLOT ASSAY WITH Mab AD6 AND TEN UNRELATED NONTYPABLE *HAEMOPHILUS INFLUENZAE*

FIG.23